

FIG. 1a

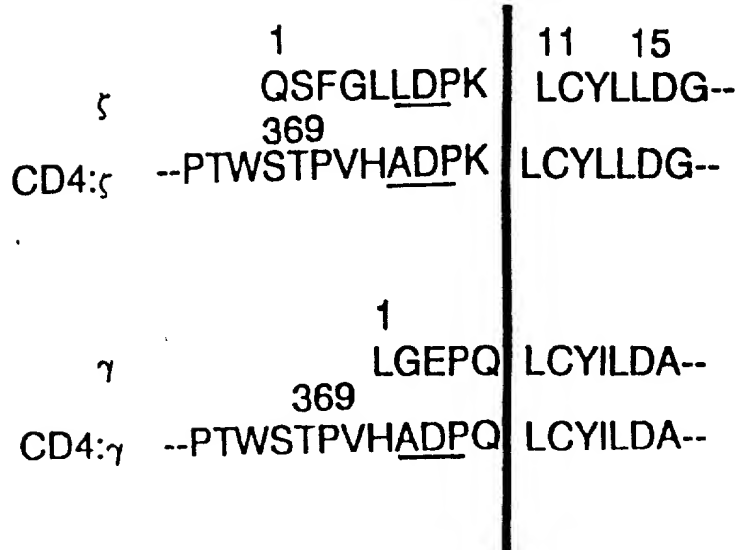


FIG. 1b

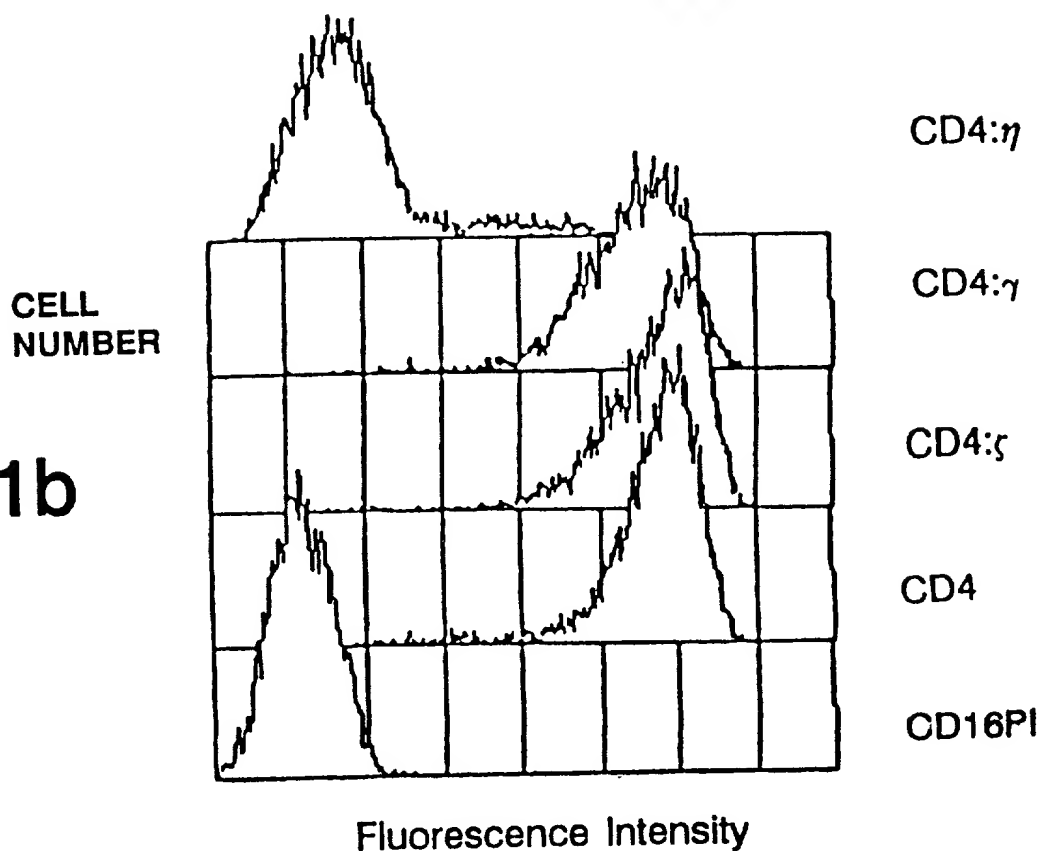


FIG. 2

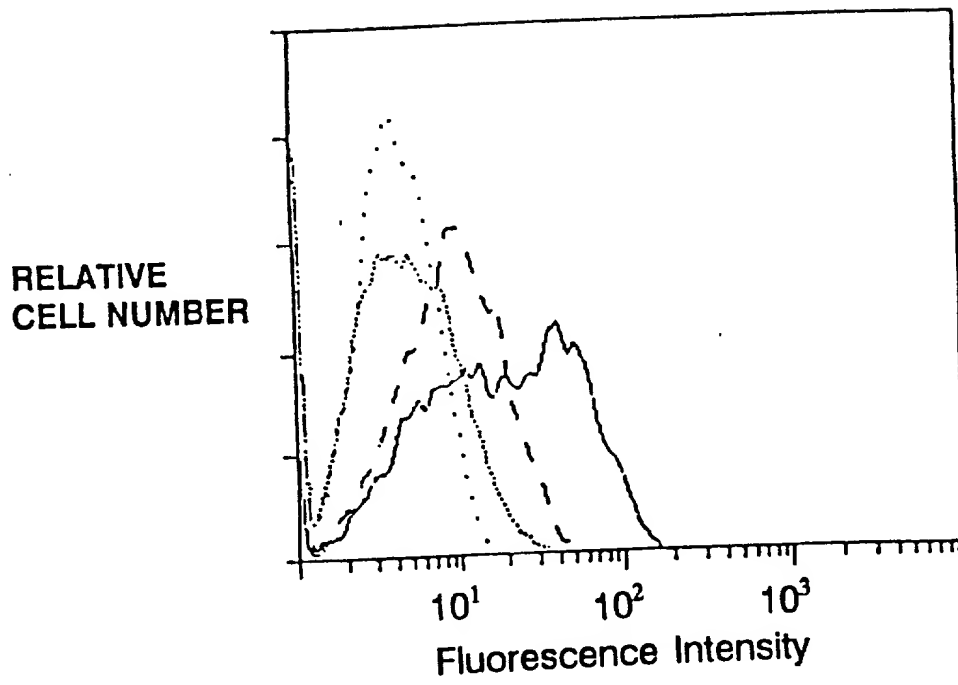


FIG. 3

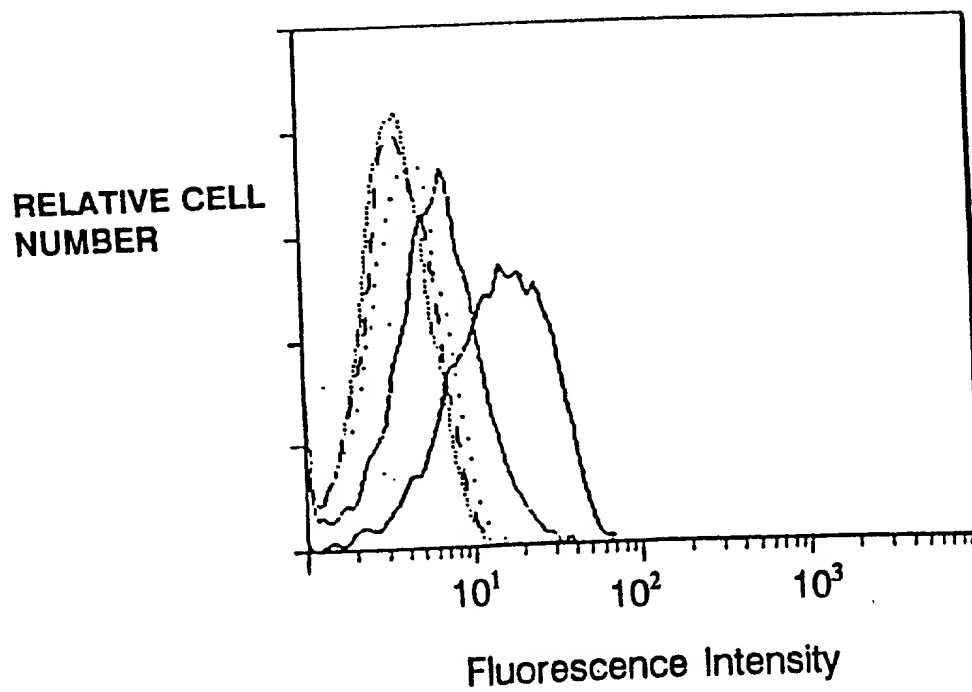


FIG. 4a

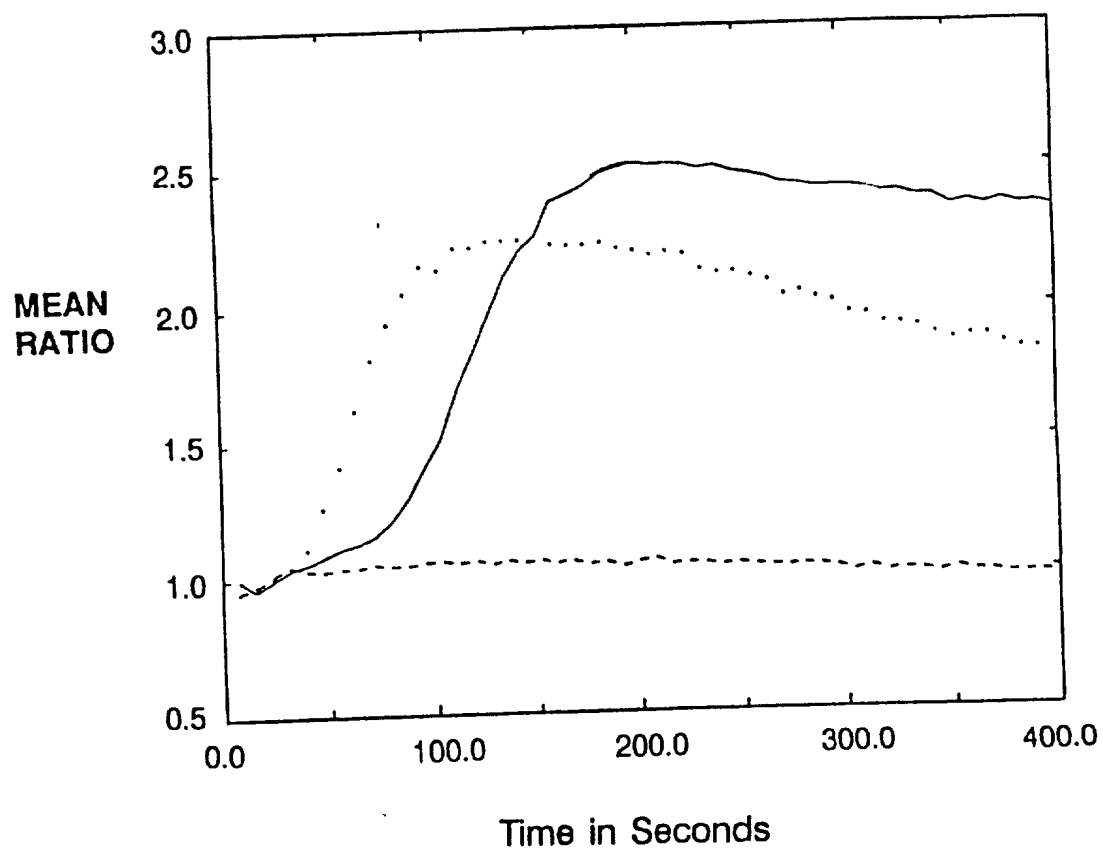


FIG. 4b

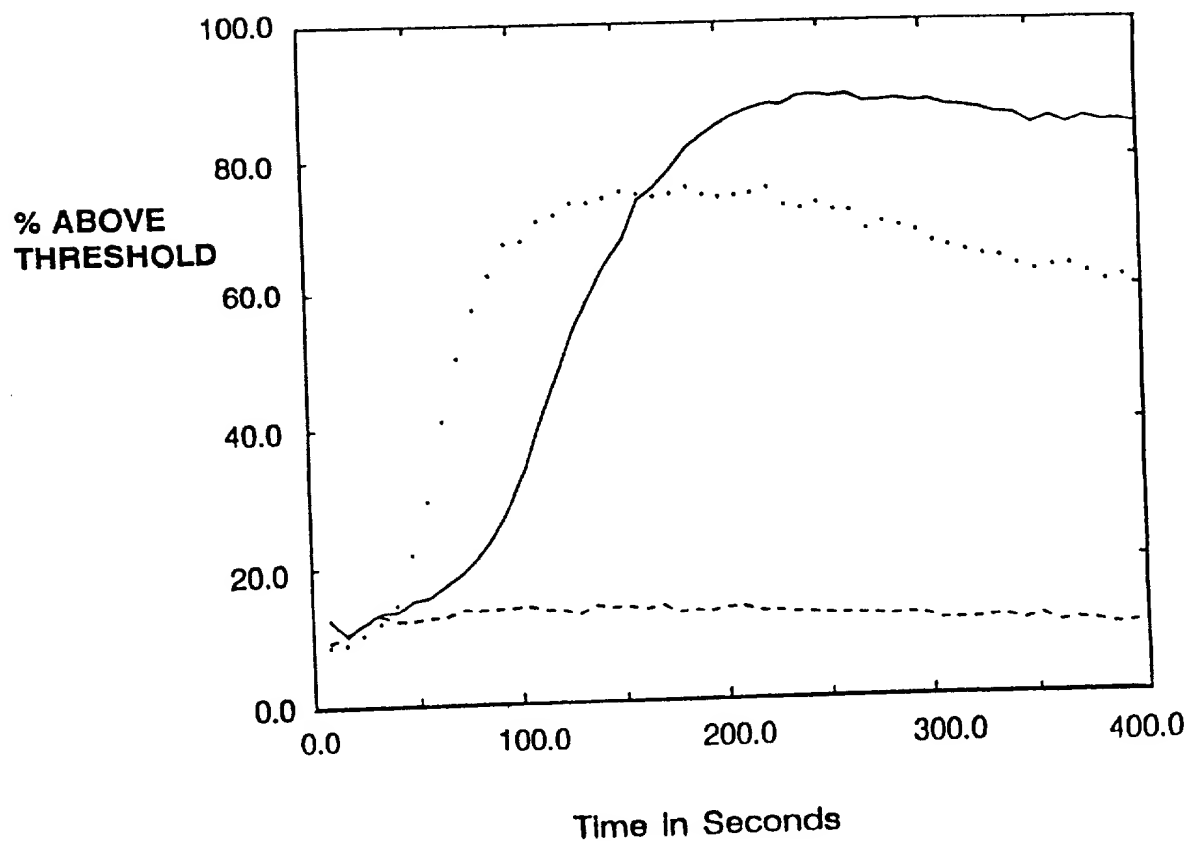


FIG. 4c

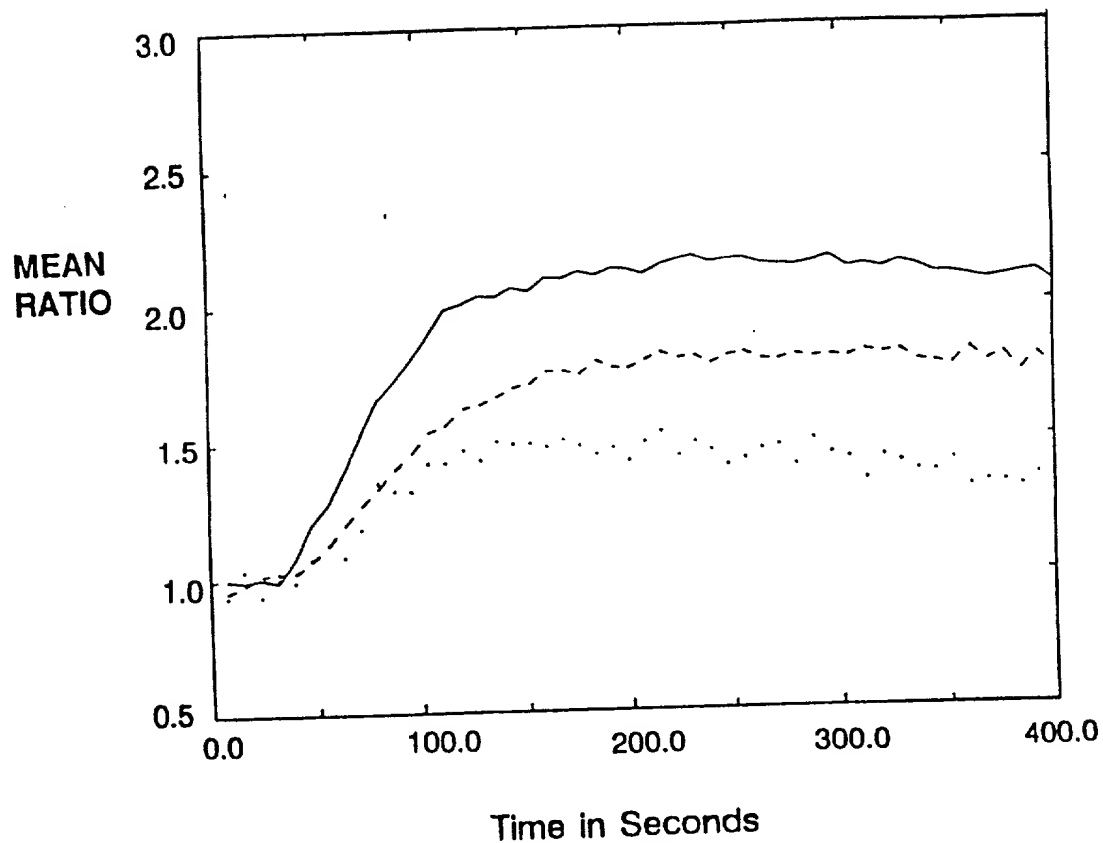


FIG. 4d

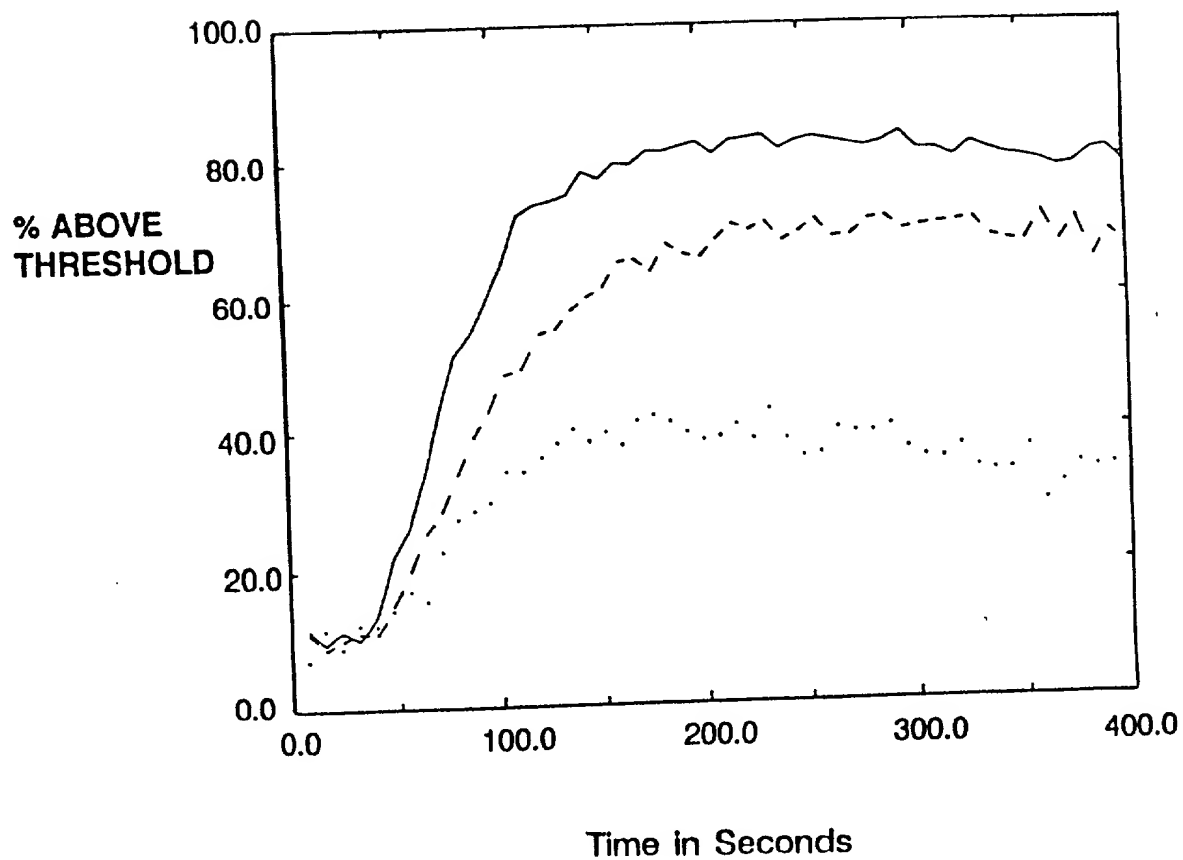


FIG. 5a

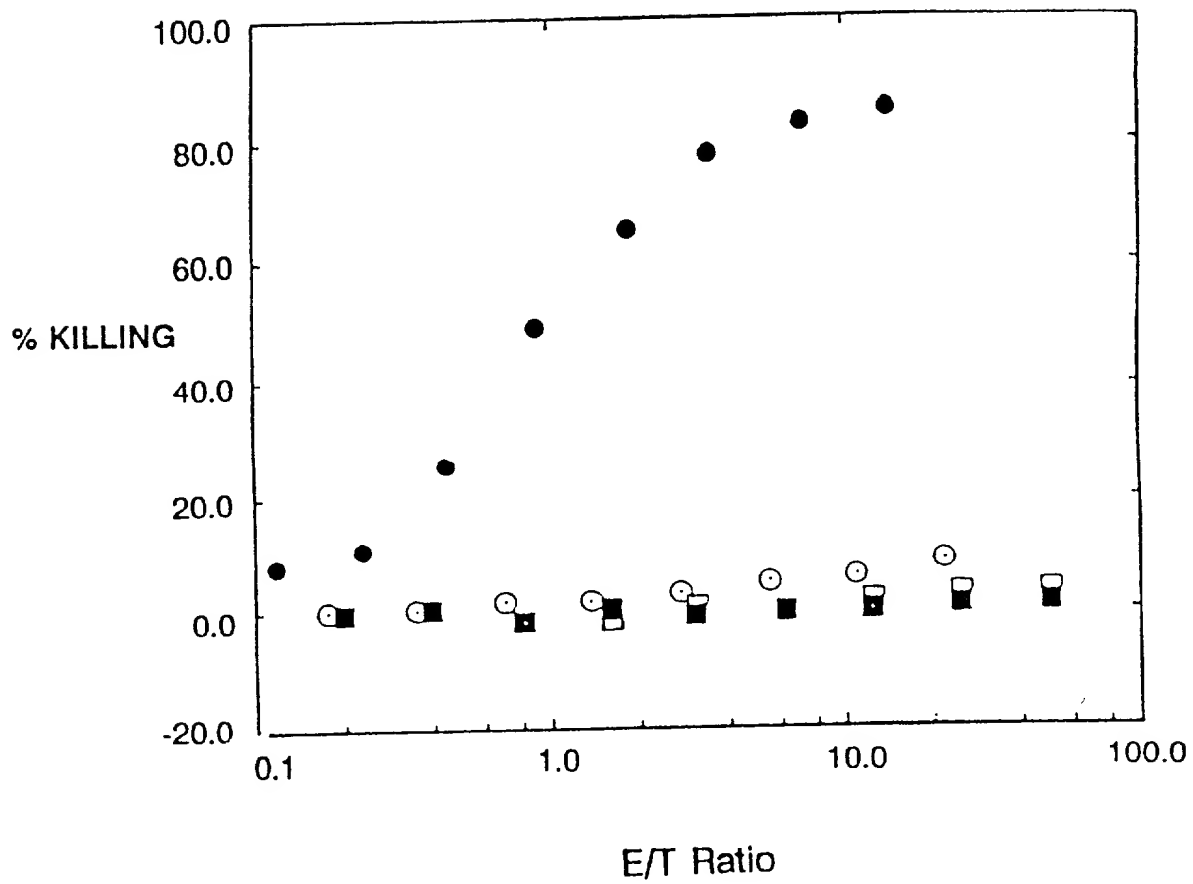


FIG. 5b

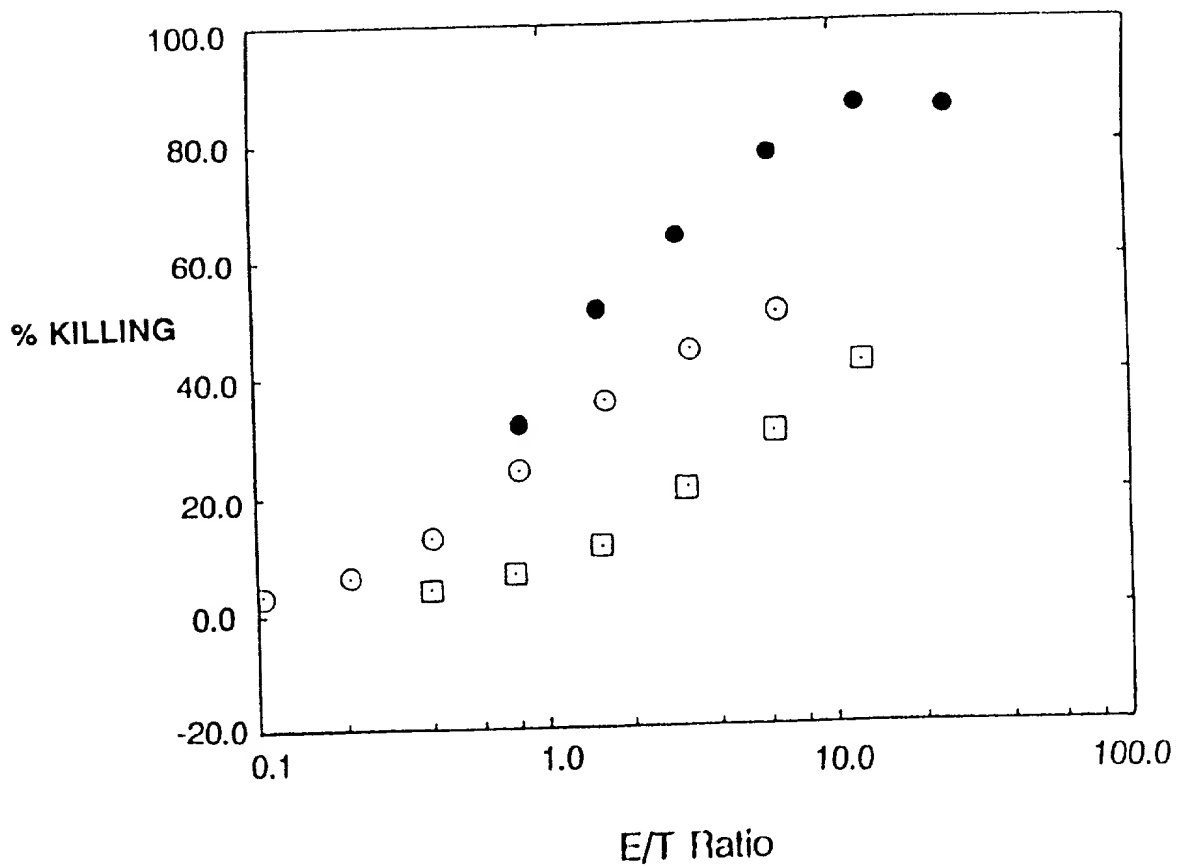


FIG. 5c

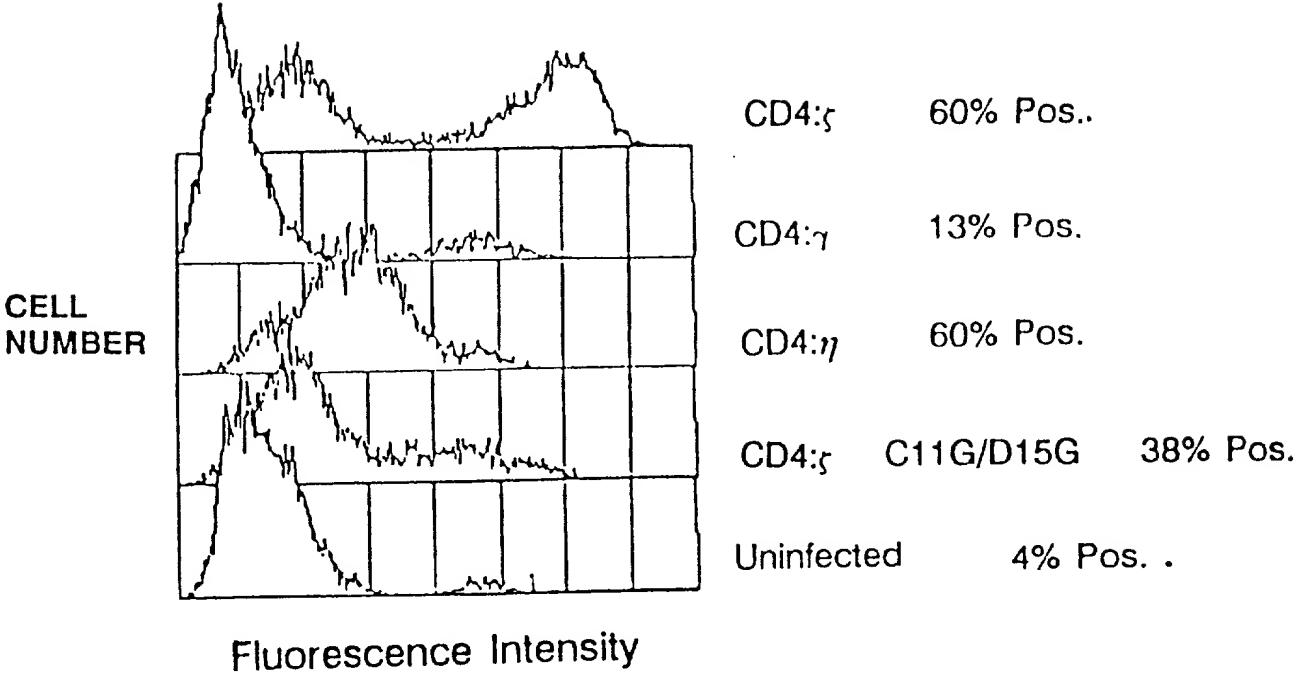


FIG. 5c

FIG. 6a

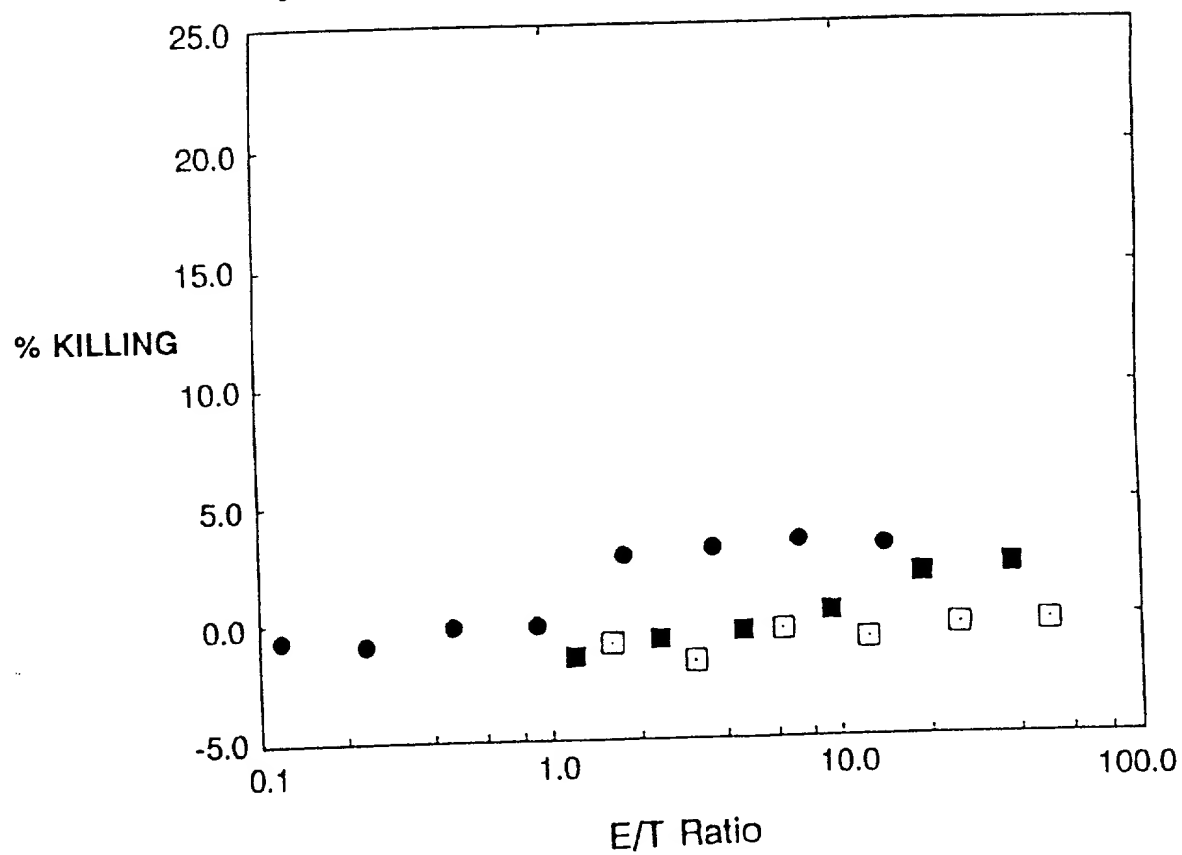


FIG. 6b

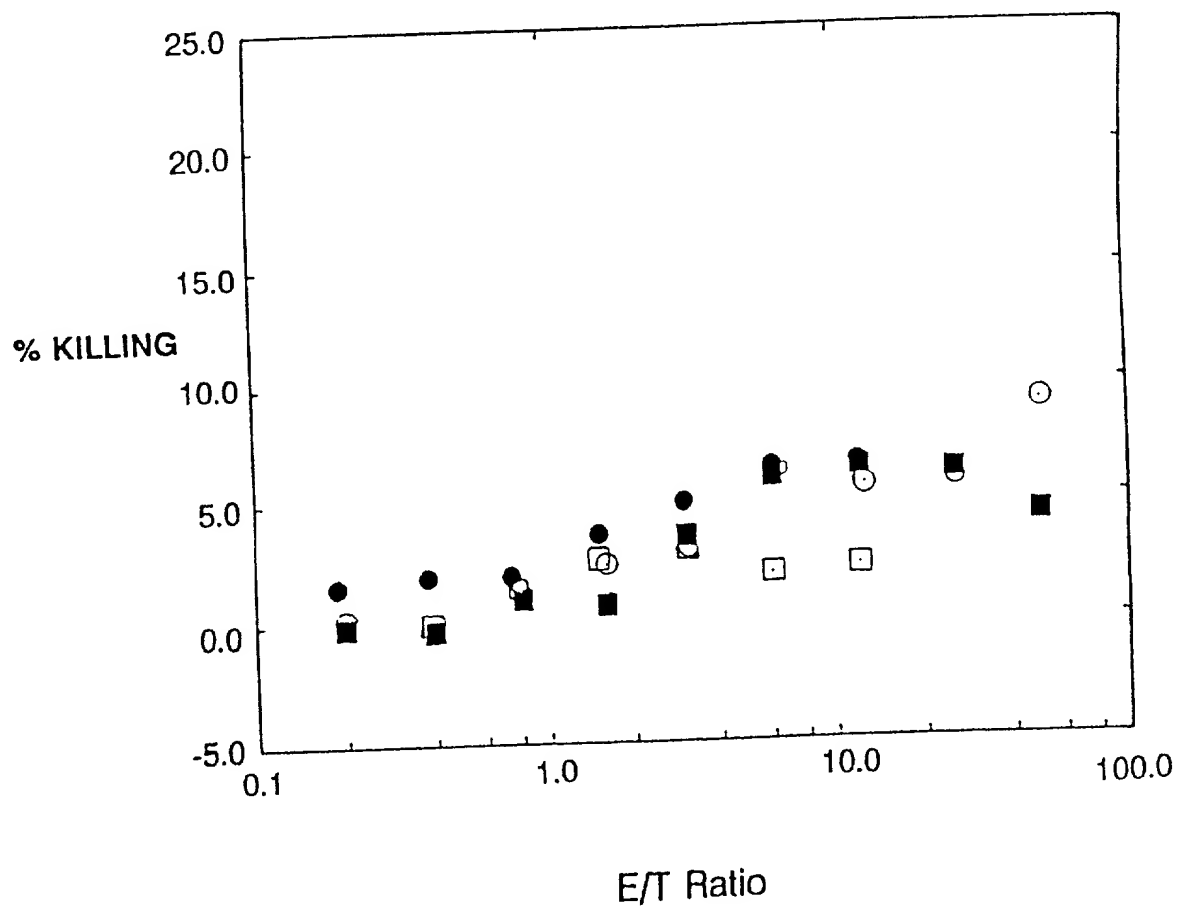


FIG. 7a

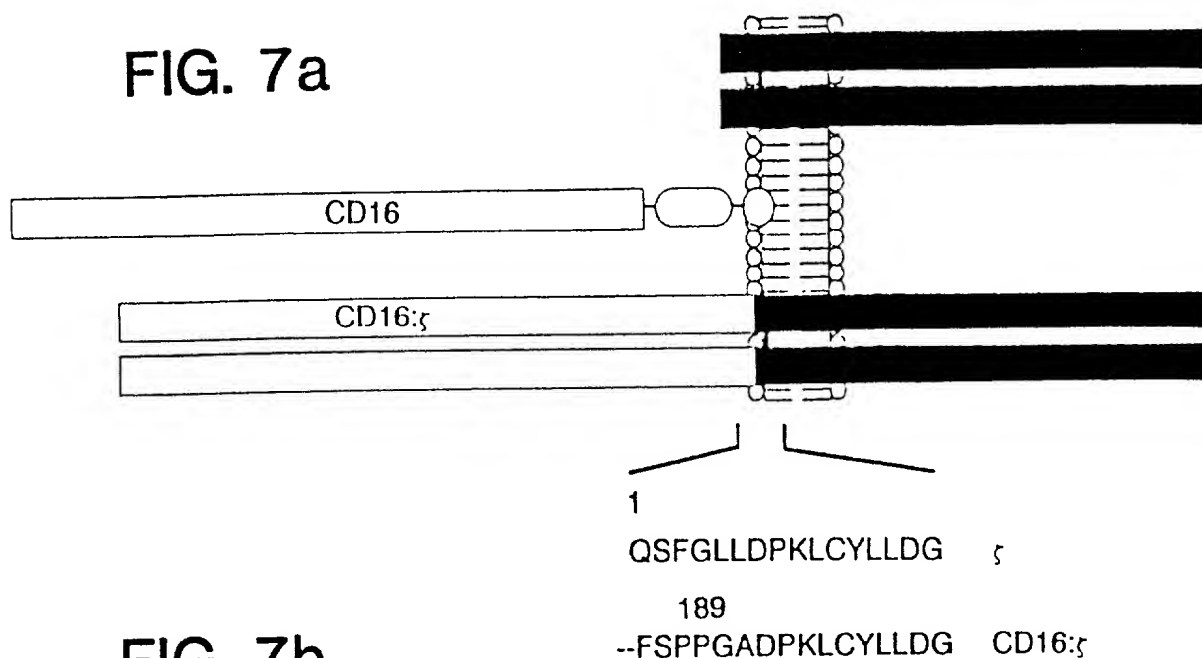


FIG. 7b

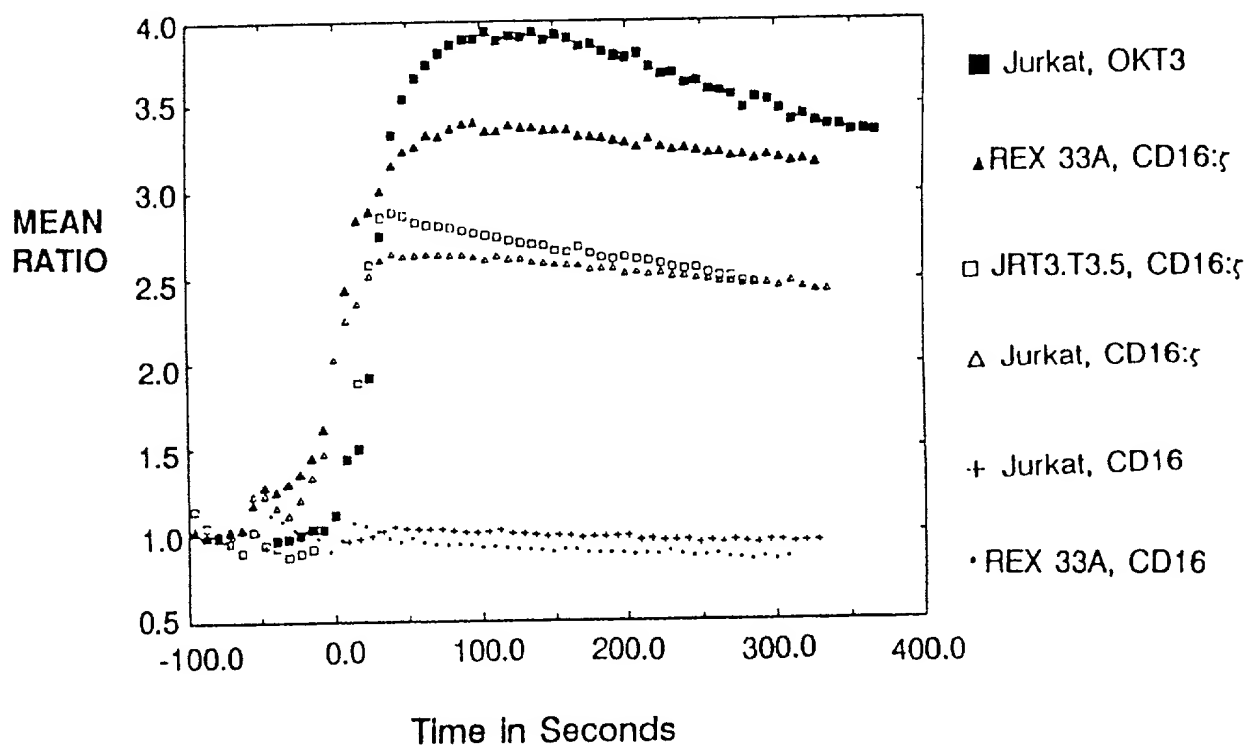


FIG. 8a

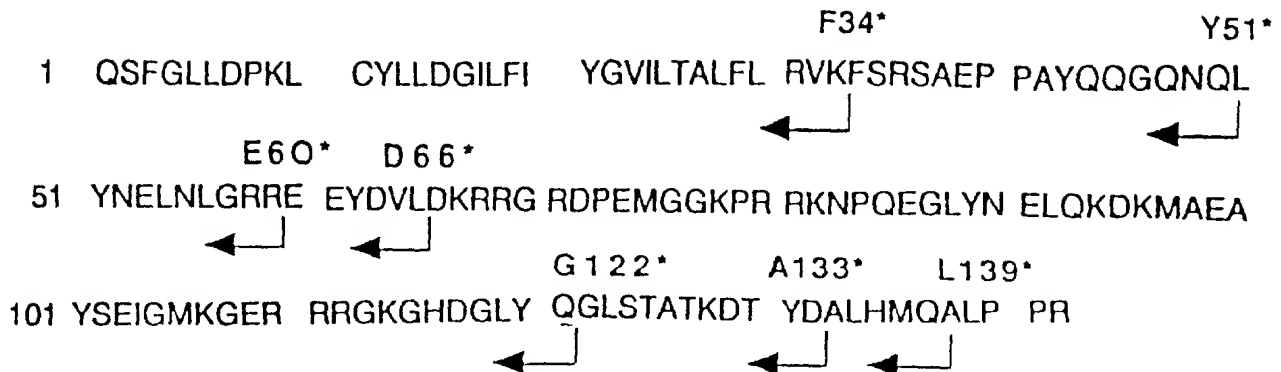


FIG. 8b

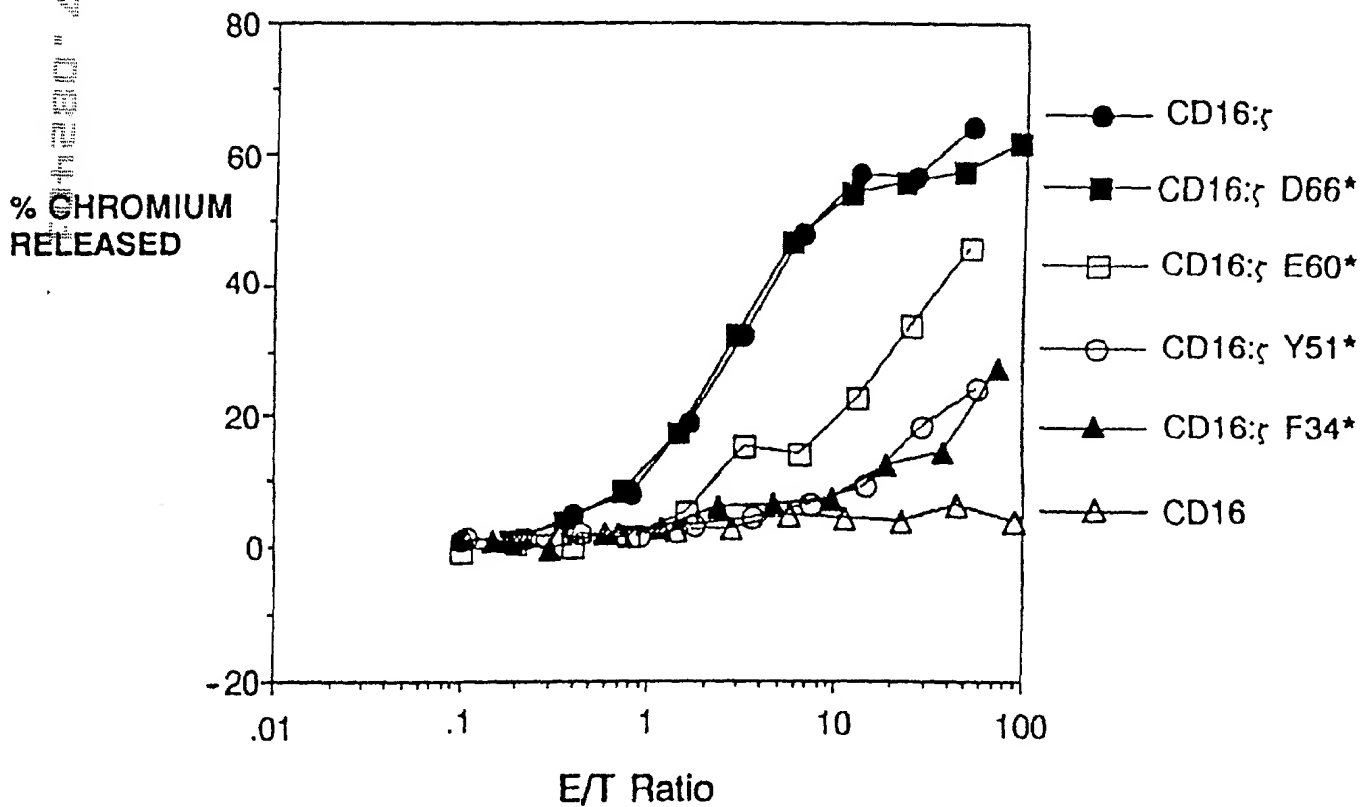


FIG. 9a

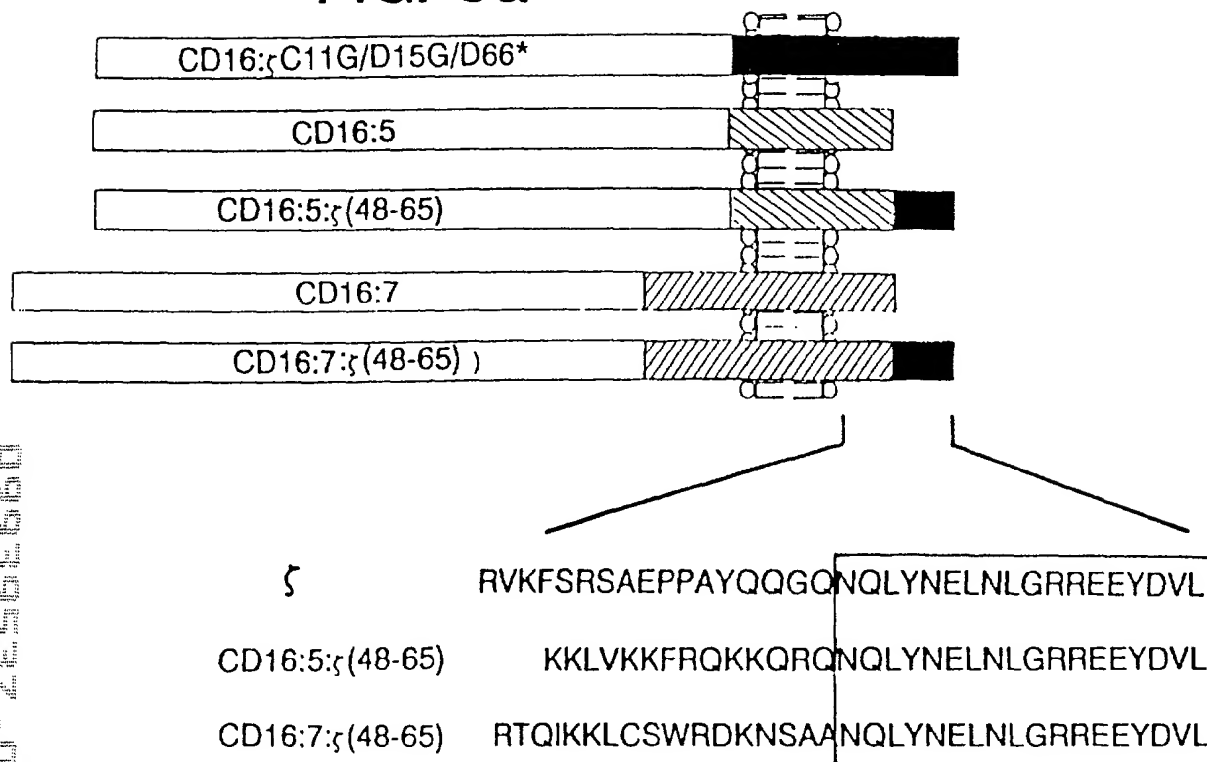


FIG. 9b

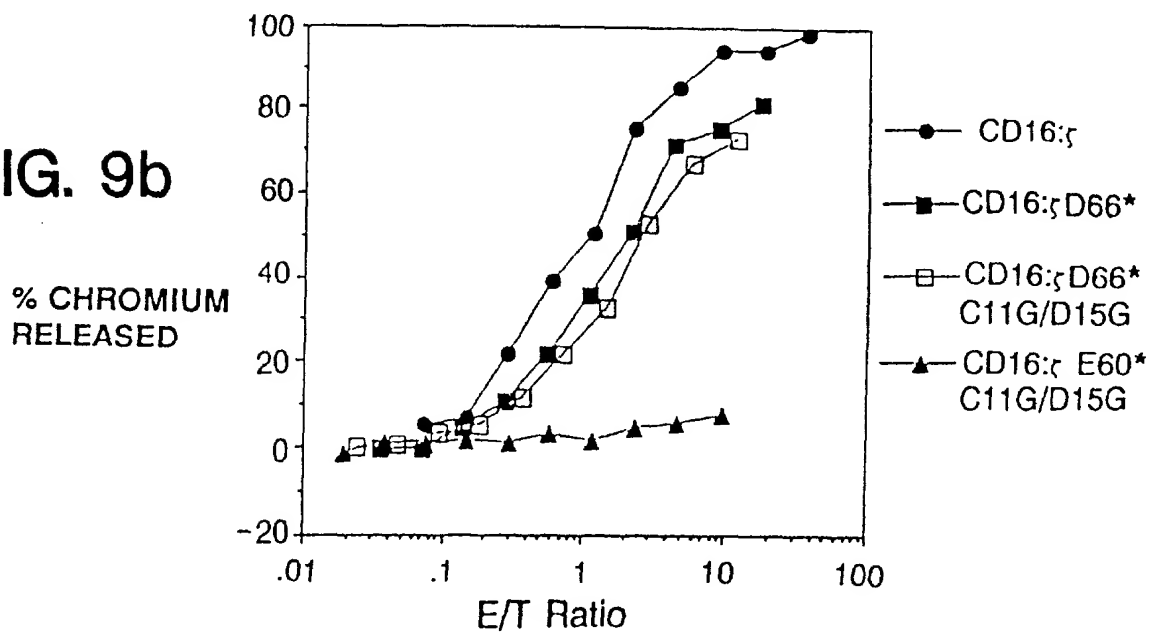


FIG. 9c

FIG. 9c

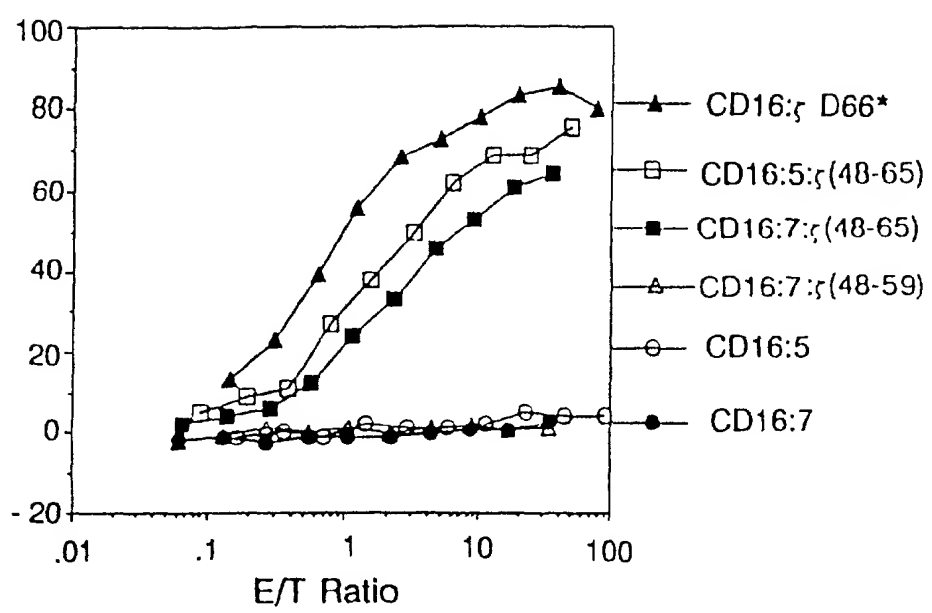


FIG. 9d

MEAN
RATIO

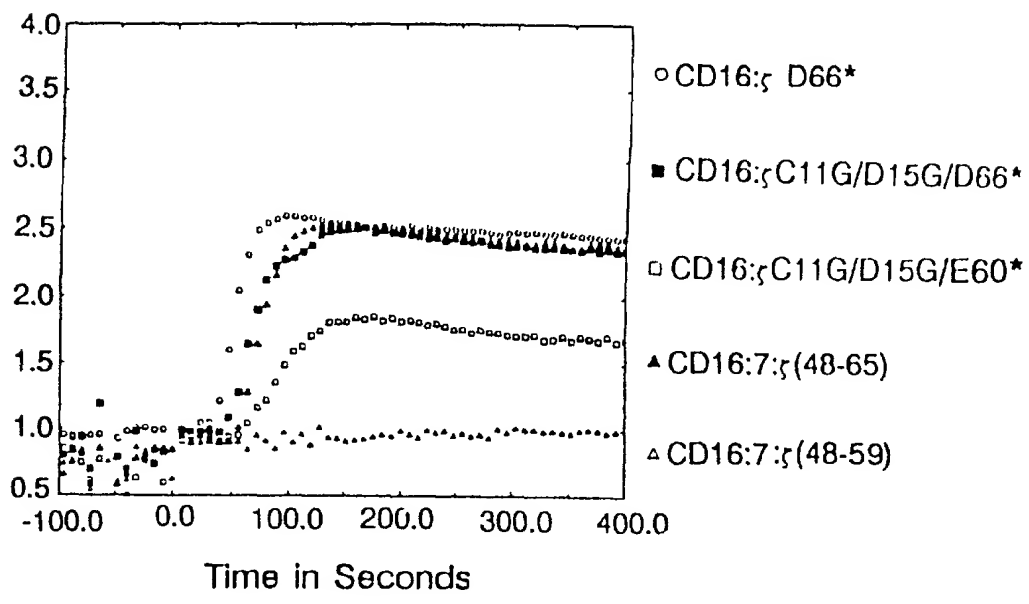


FIG. 10a

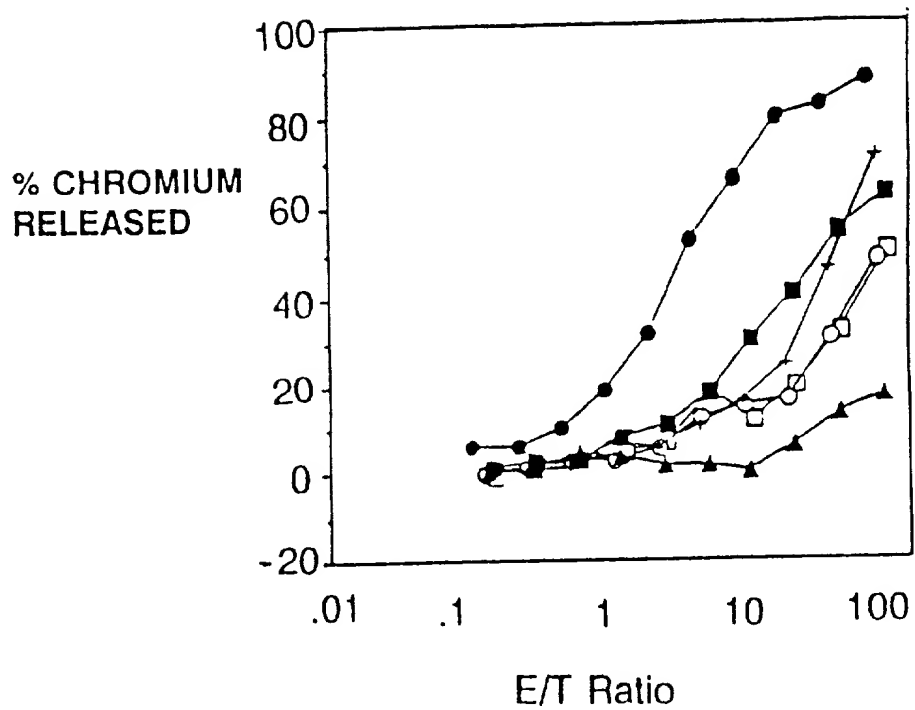


FIG. 10b

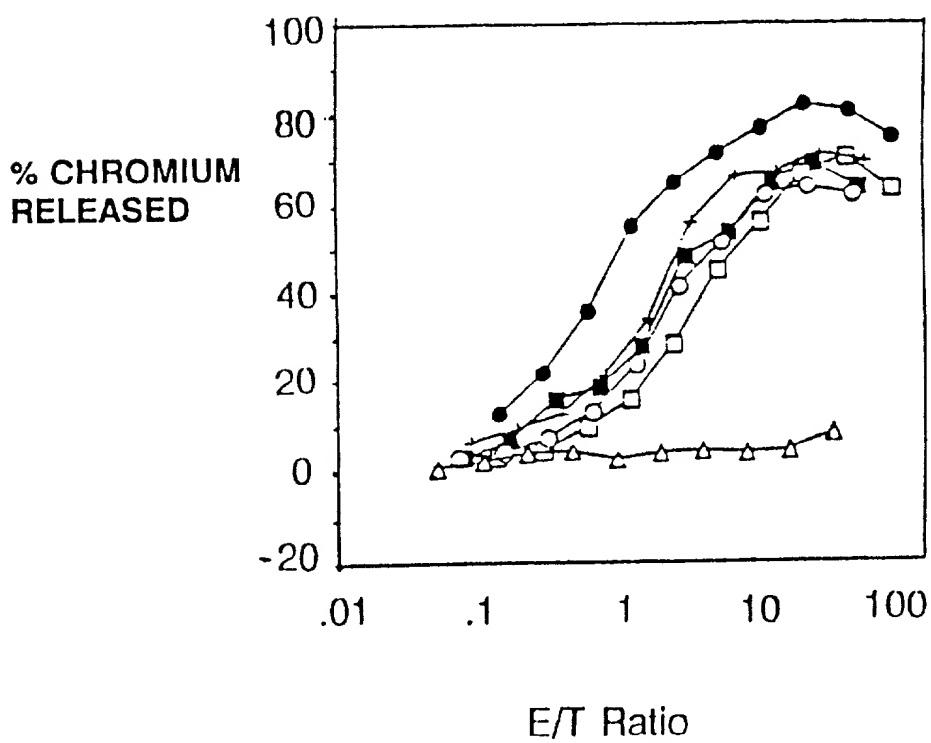


FIG. 10c

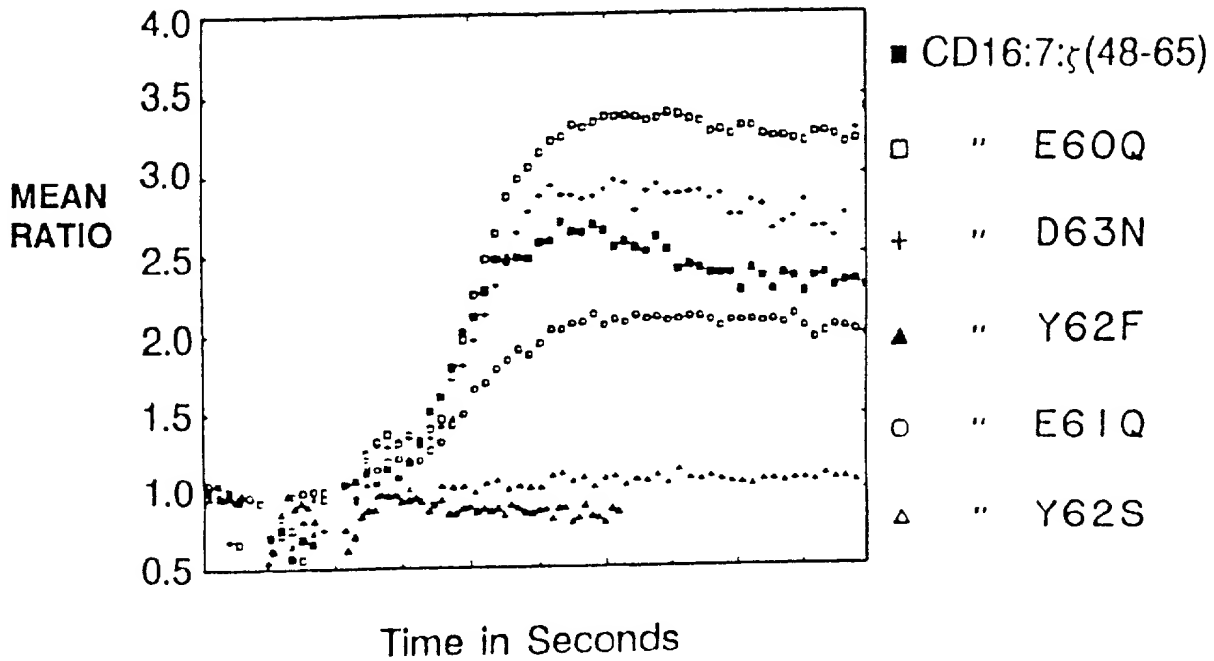
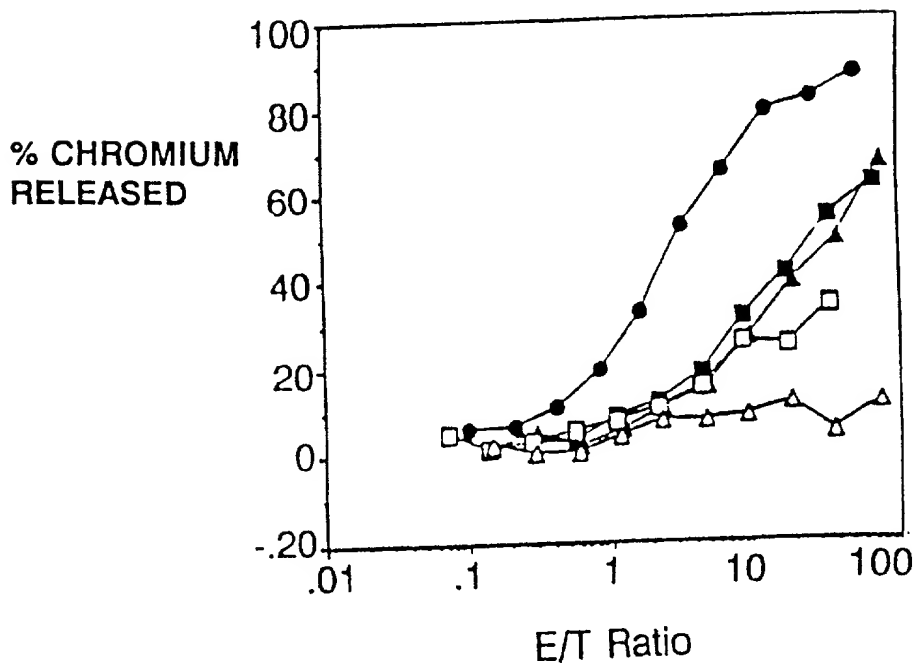


FIG. 10d



● FIG. 10e ●

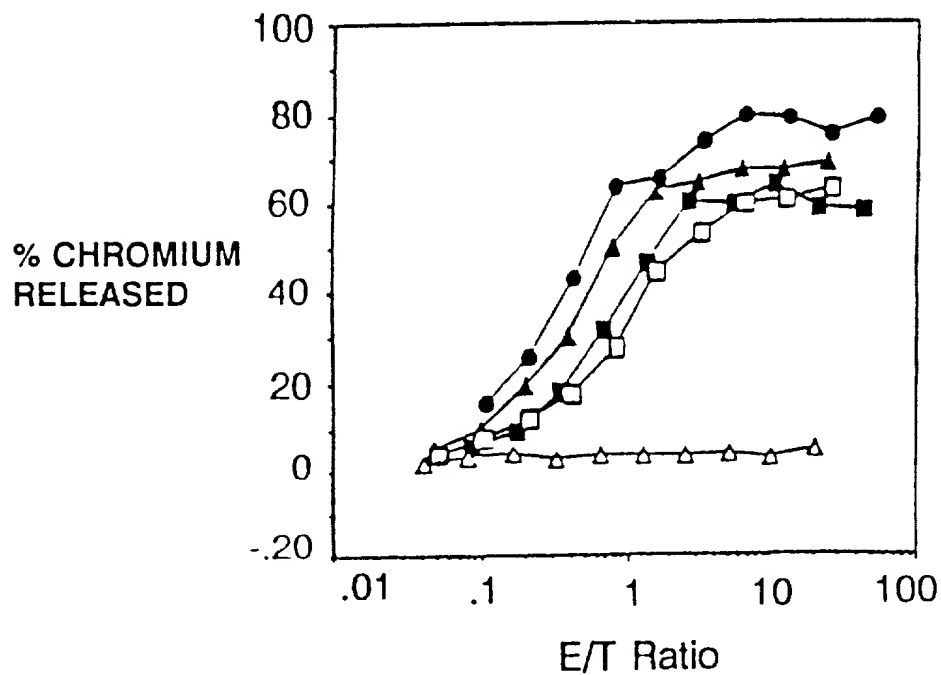


FIG. 10f

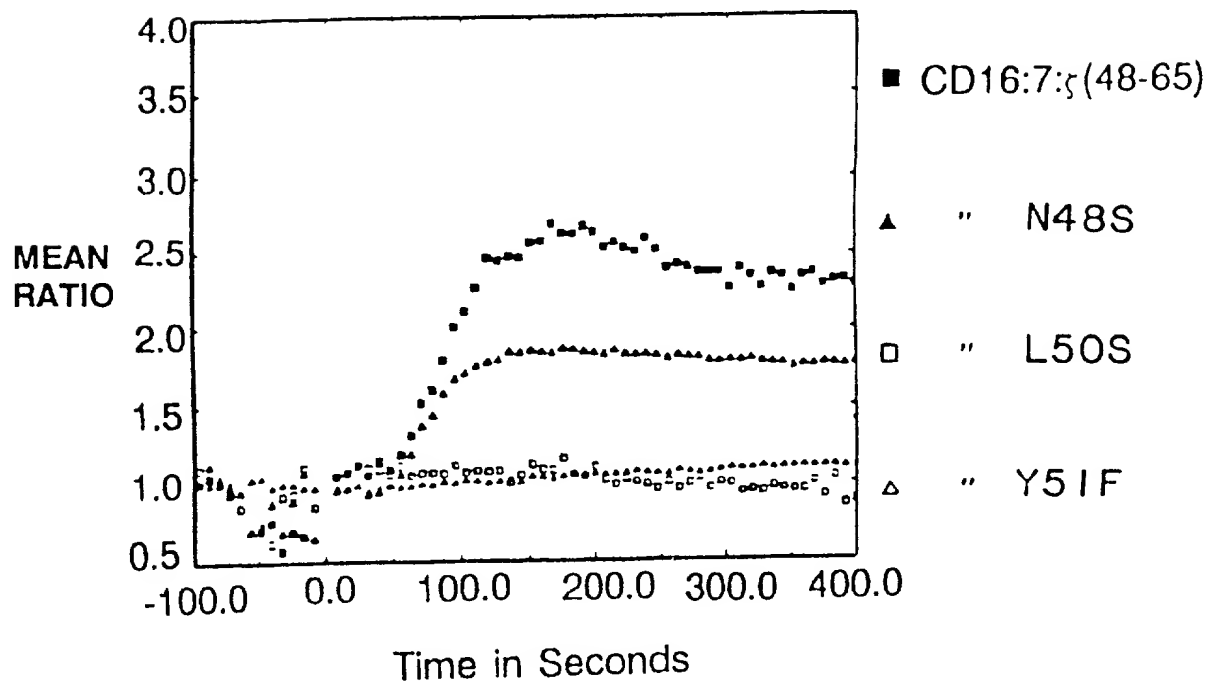


FIG. 11a

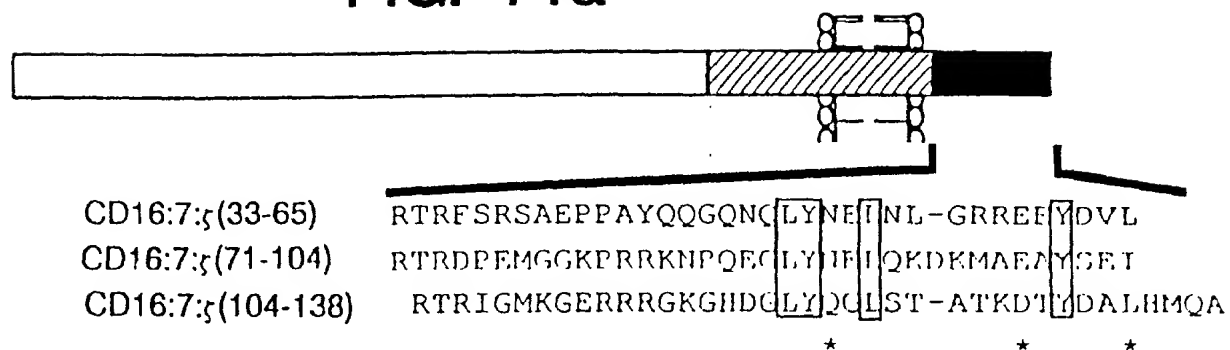


FIG. 11b

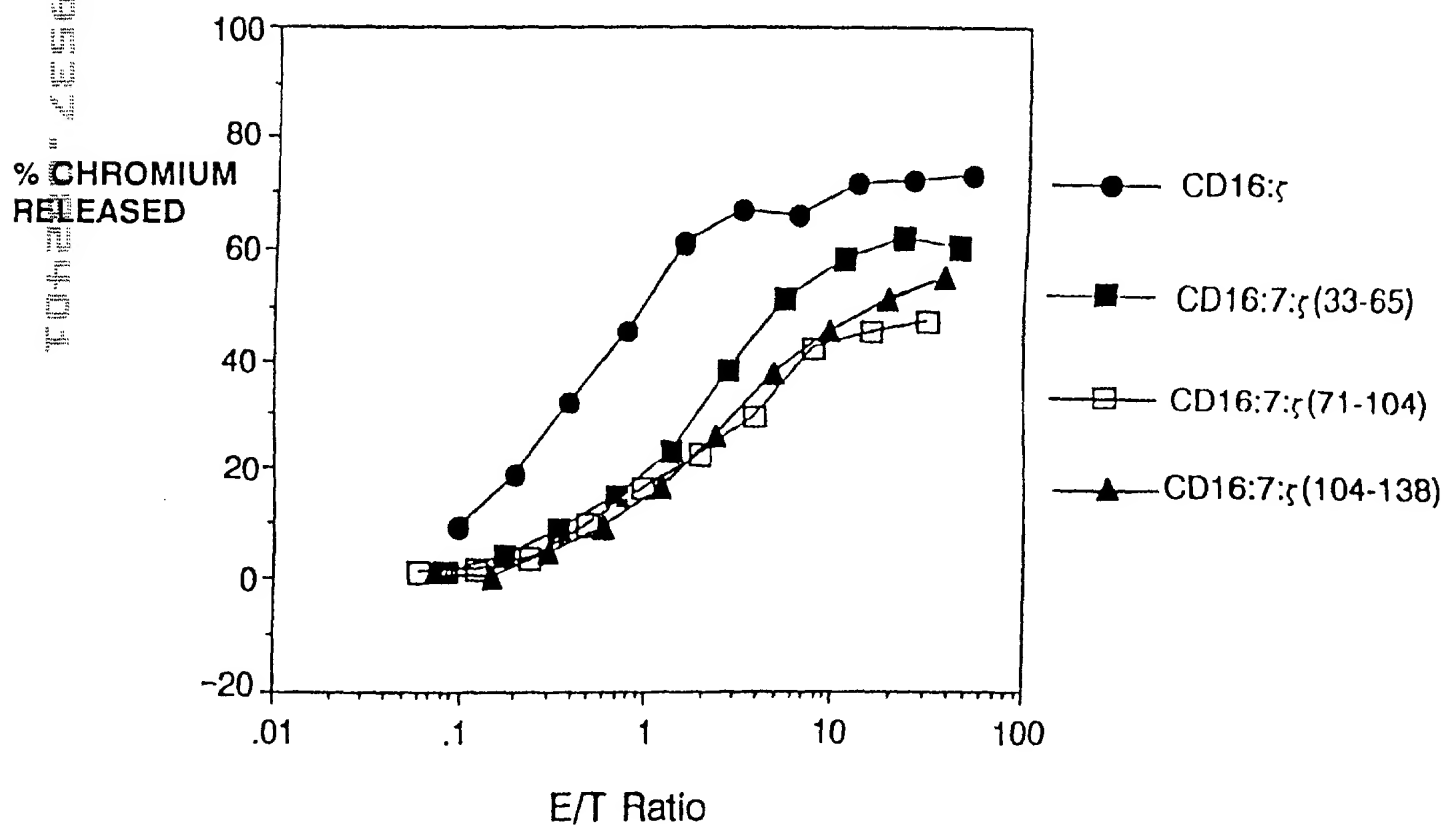


FIG. 12

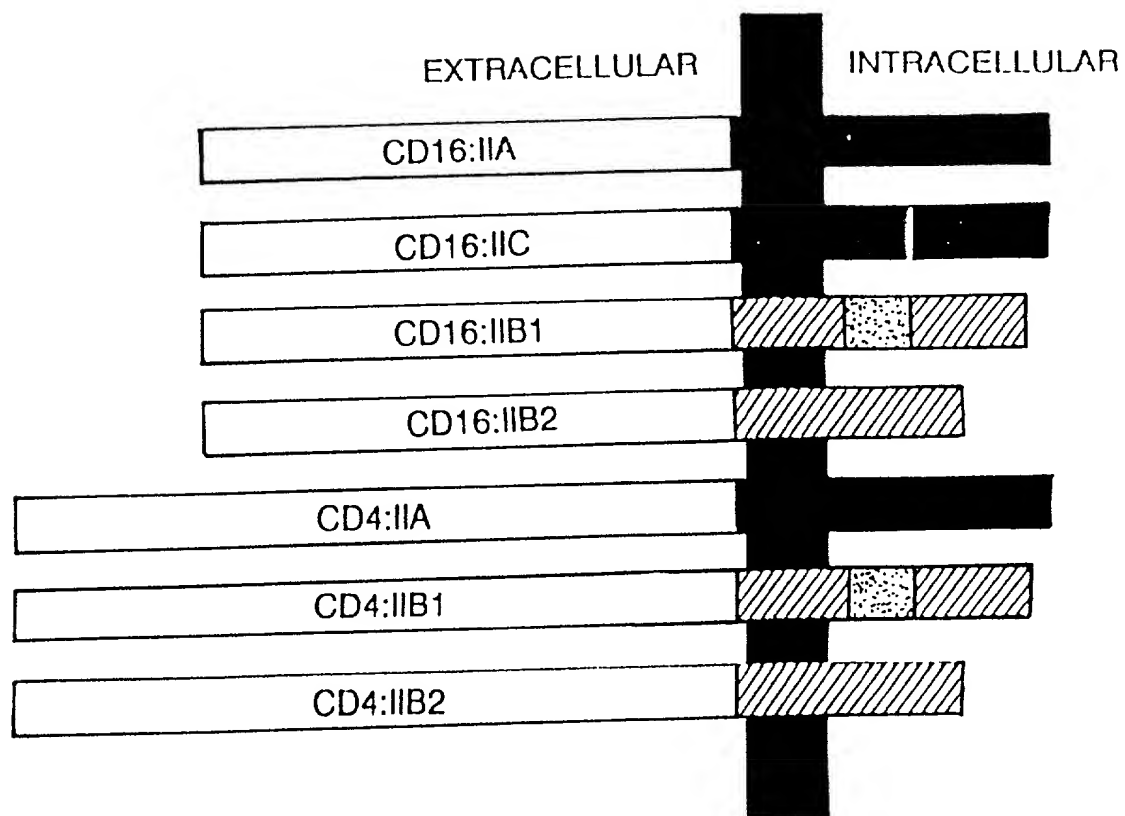


FIG. 12

FIG. 13a

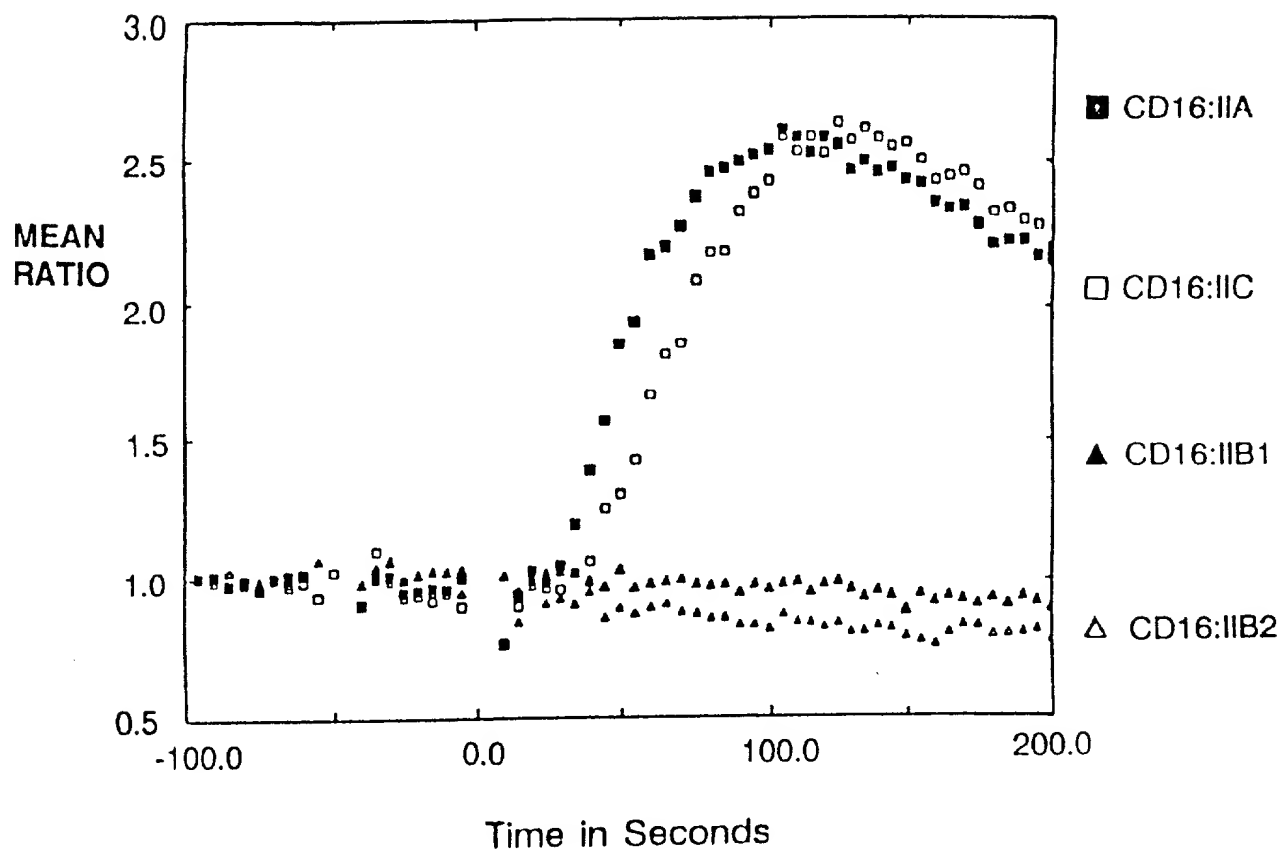


FIG. 13b

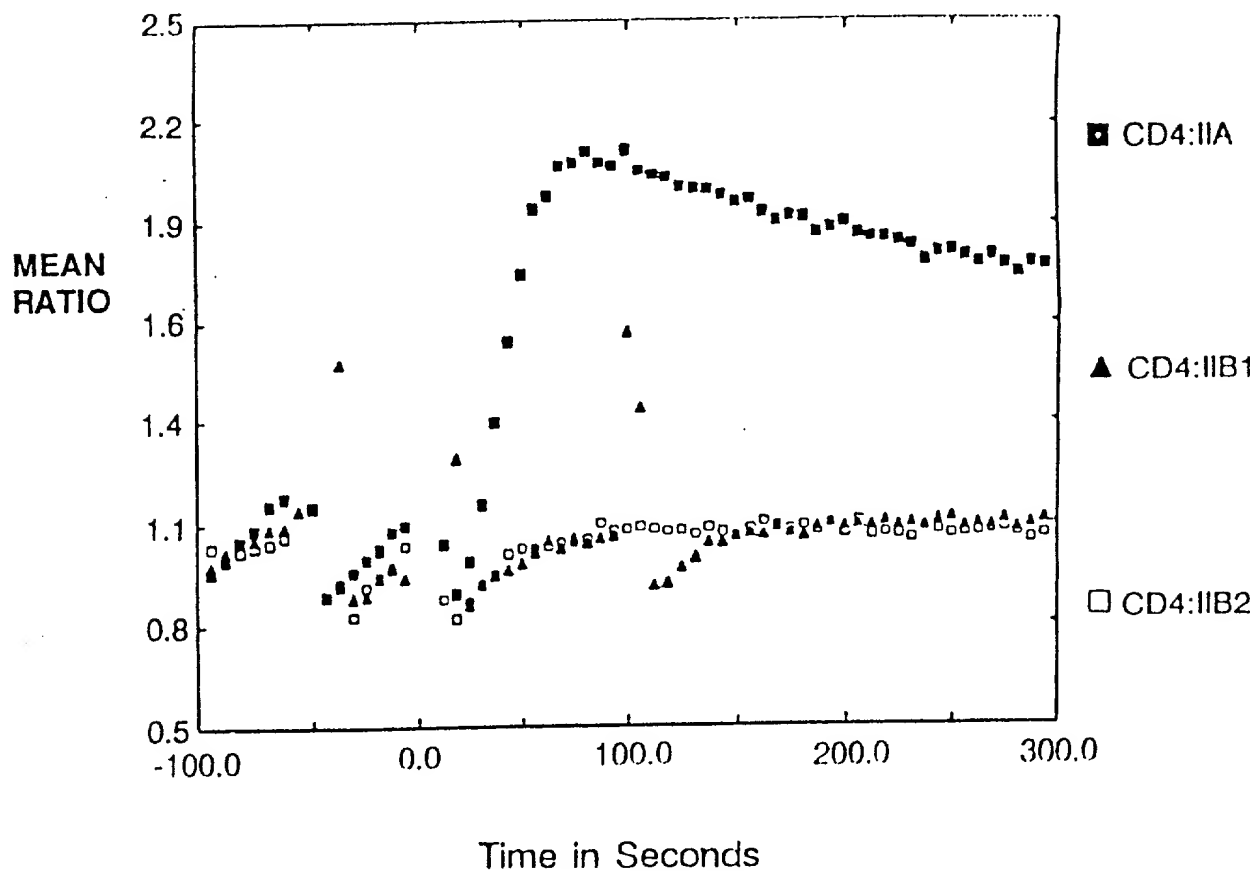


FIG. 14a

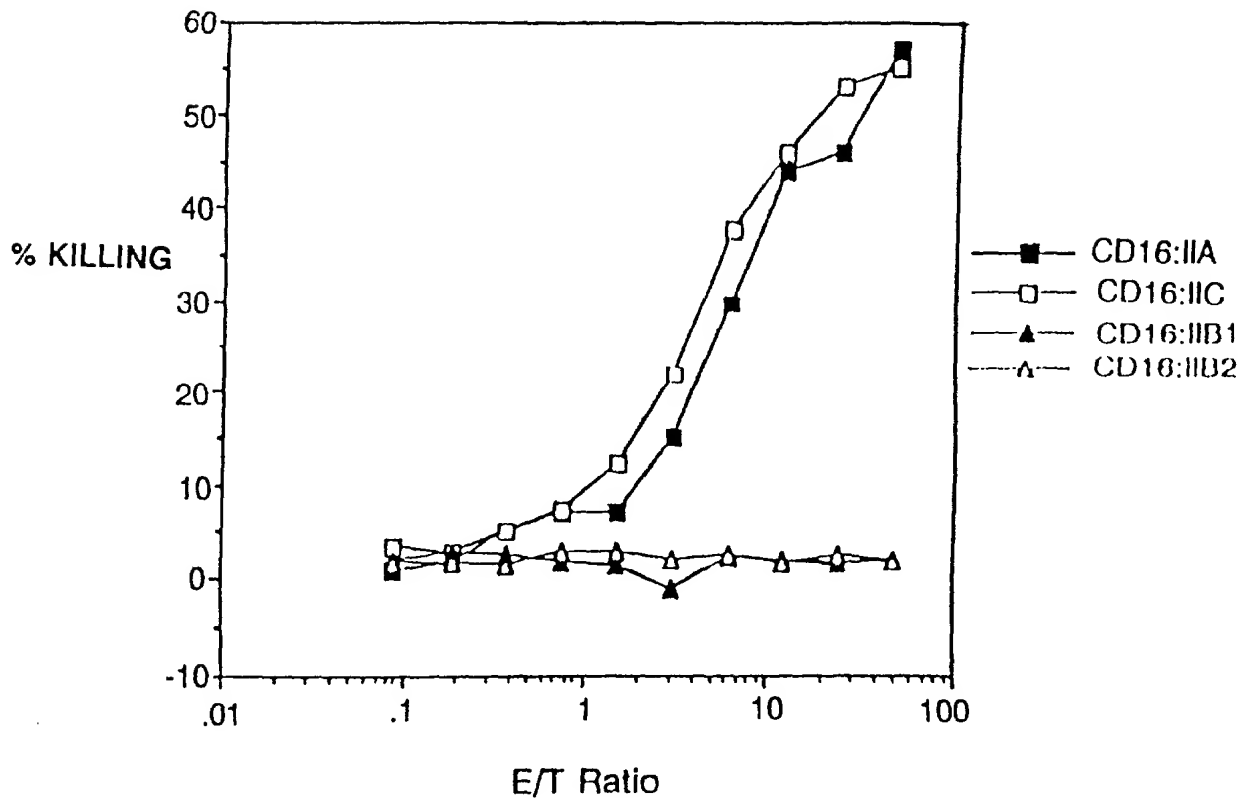


FIG. 14b

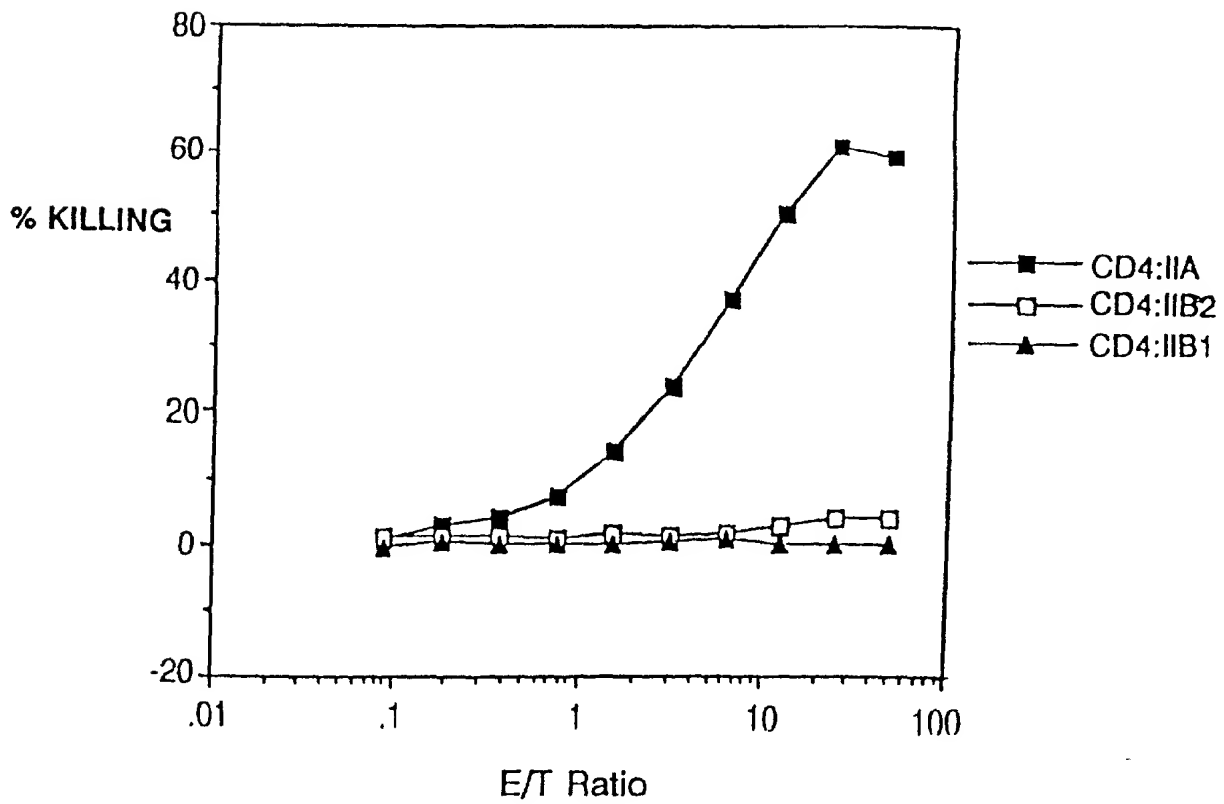


FIG. 15a

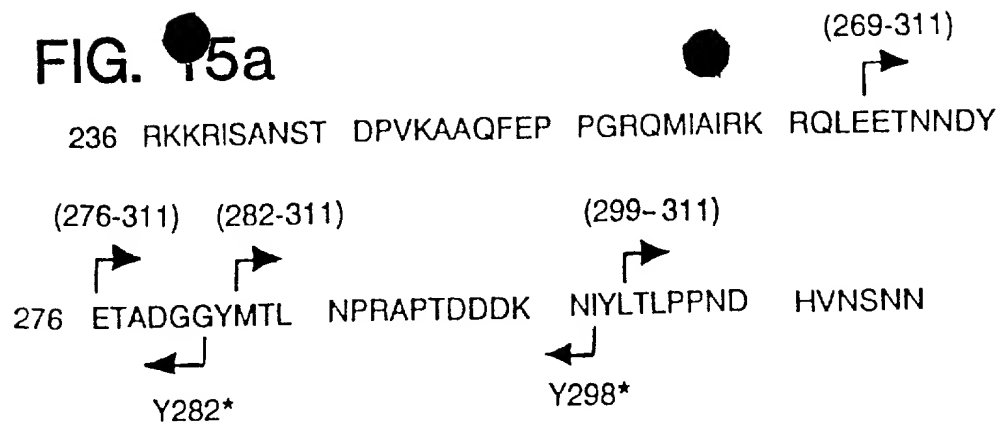


FIG. 15b

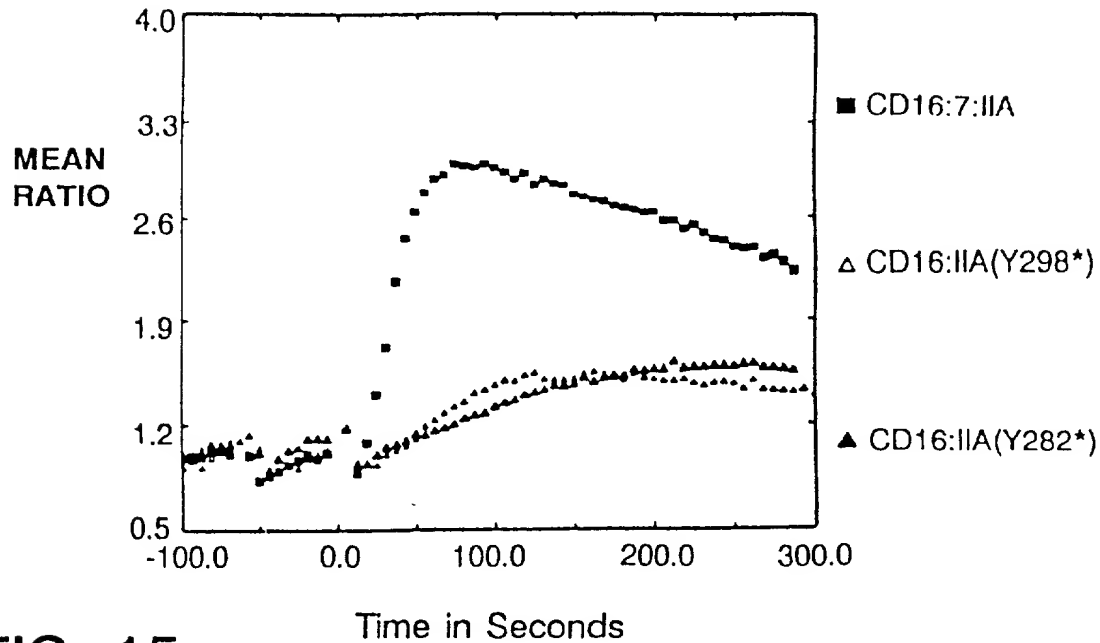


FIG. 15c

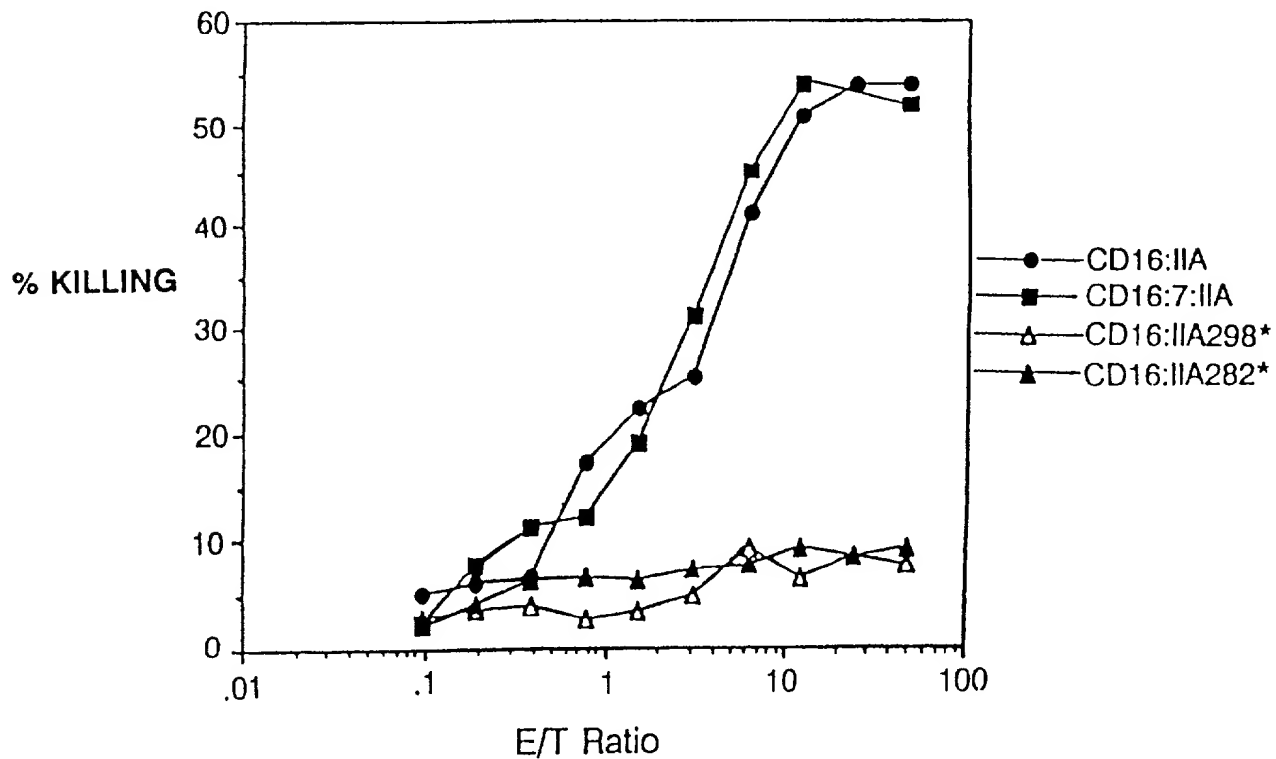


FIG. 15d

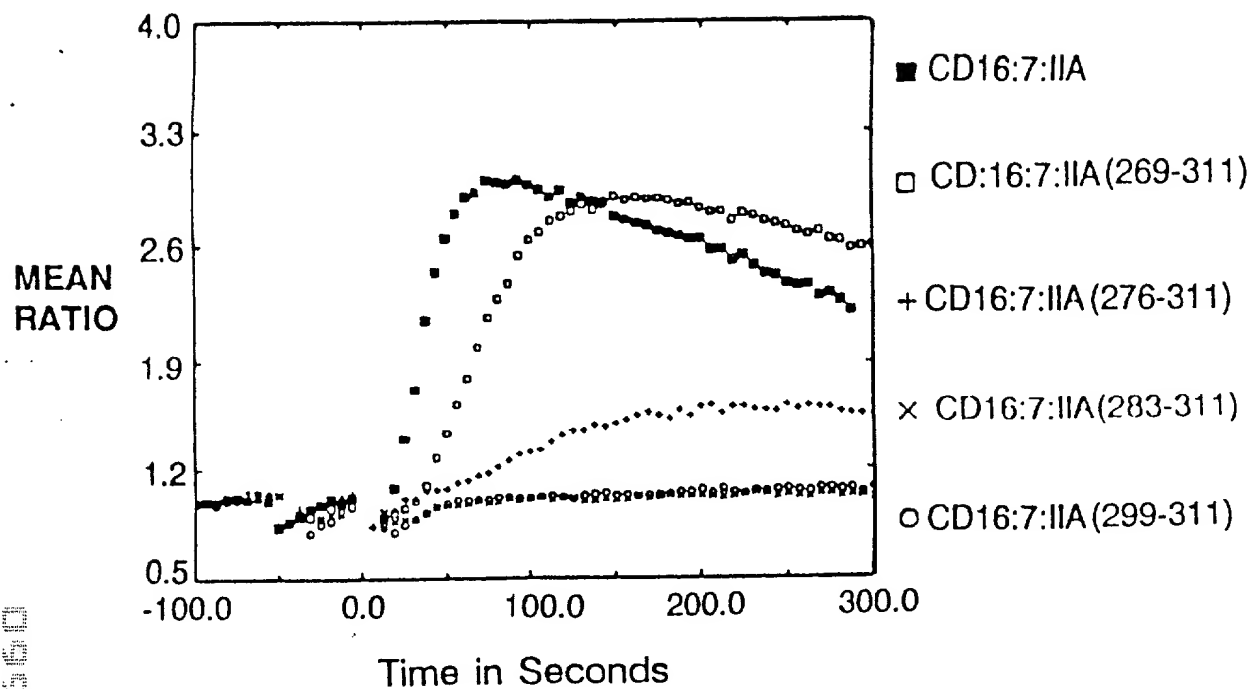


FIG. 15e

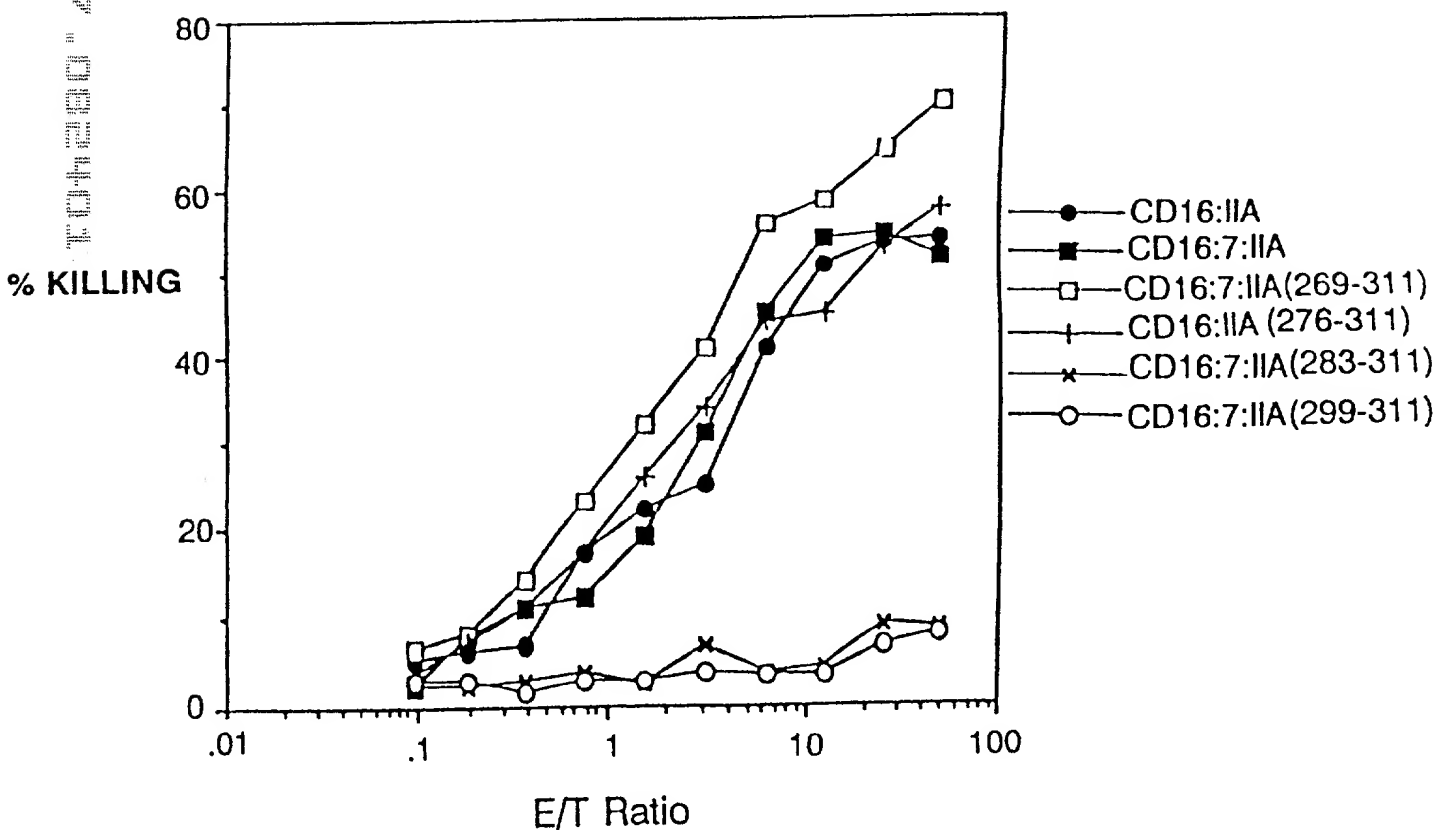


FIG.16 (Seq. ID No: 24)

1 MEHSTFLSGL VLATLLSQVS PFKIPIEELE DRVFNVCNTS ITWVEGTVGT
 51 LLSDITRLDL GKRILDPRGI YRCNGTDIYK DKESTVQVHY RMCQSCVELD
 101 PATVAGIIVT DVIATLLLAL GVFCFAGHET GRLSGAADTQ ALLRNDQVYQ
 151 PLRDRDDAQY SHLGGNWARN K*

FIG.17 (Seq ID NO: 25)

1 MEQGKGLAVL ILAIILLQGT LAQSIKGNHL VKVYDYQEDG SVLLTCDAEA
 51 KNITWFKDGK MIGFLTEDKK KWNLGSKAKD PRGMYQCKGS QNKSKPLQVY
 101 YRMCQNCIEL NAATISGFLF AEIVSIFVLA VGVYFIAGQD GVRQSRASDK
 151 QTLFPNDQLY QPLKDREDDQ YSHLQGNQLR RN*

FIG.18 (Seq ID No: 26)

1 MPGGLEALRA LPLLLFLSYA CLGPGCQALR VEGGPPSLTV NLGEEARLTC
 51 ENNGRNPNTT WWFSLQSNIT WPPVPLGPGQ GTTGQLFFPE VNKNTGACTG
 101 CQVIENNILK RSCGTYLRVR NPVPRPFLLM GEGTKNRIIT AEGIILLFCA
 151 VVPGTLLLFR KRWQNEKFGV DMPDDYEDEN LYEGLNLDDC SMYEDISRGL
 201 QGTYQDVGNL HIGDAQLEKP *

FIG.19 (Seq ID No: 27)

1 MATLVLSMP CHWLLFLLLL FSGEPVPAMT SSDLPLNFQG SPCSQIWQHP
 51 RFAAKKRSSM VKFHCTNHS GALTWFRKRG SQQPQELVSE EGRIVQTQNG
 101 SVYTLTIQNI QYEDNGIYFC KQKCDSANHN VTDSCGTELL VLGFTSLDQL
 151 KRRNTLKDGI ILIQTLIIIL FIIVPIFLLL DKDDGKAGME EDHTYEGLNI
 201 DQTATYEDIV TLRTGEVKWS VGEHPGQE*

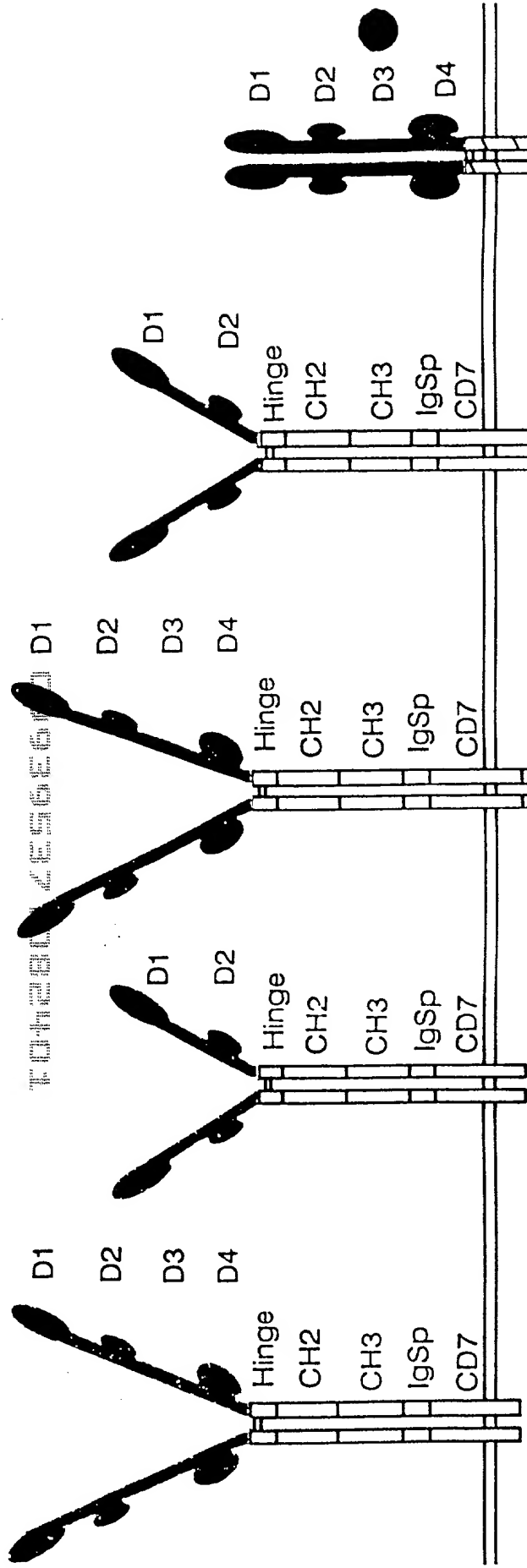


FIG. 20a

FIG. 20b

FIG. 20c

FIG. 20d

FIG. 20e

BamHI/BstY1

Bgl2/BstY1

G GAT CCC AAG GCC AGG CTA AAG CCG AAG CCG CGA AGG CCG AGG CTA AGG CCG AAG CAG ATC IG

D P K A E A K A E A K A E A K A E A D L

FIG. 28

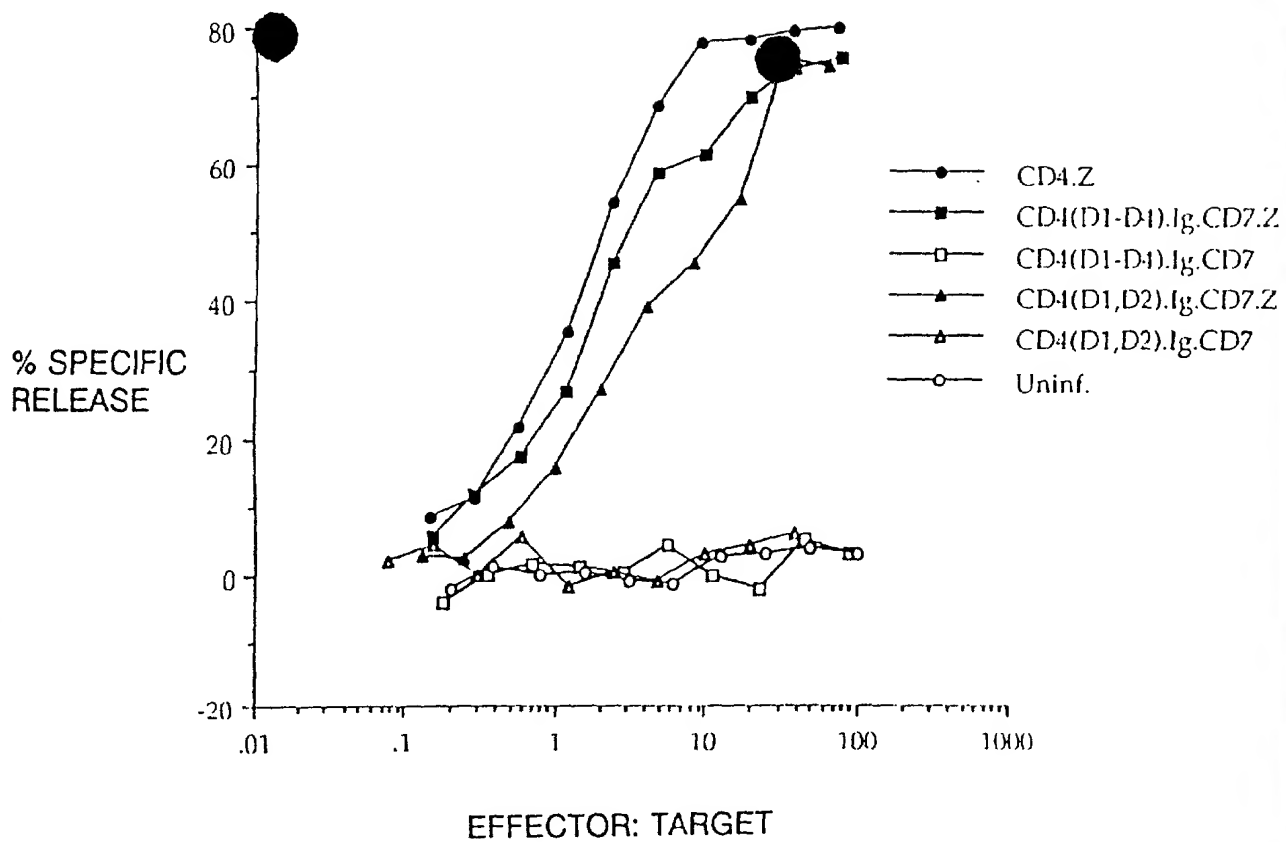


FIG. 21

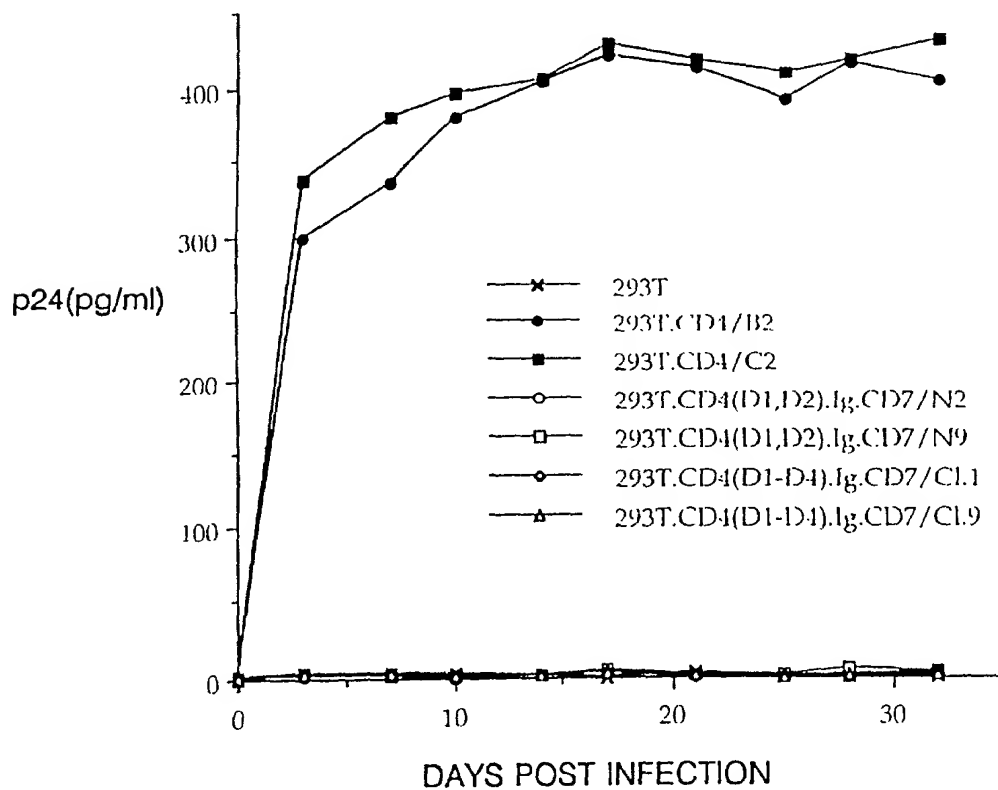


FIG. 22

Nucleic Acid Sequence

GCCTGTTTGA	GAAGCAGCGG	GCAAGAAAGA	CGCAAGCCCA	GAGGCCCTGC	51
CATTTCTGTG	GGCTCAGGTC	CCTACTGGCT	CAGGCCCTTG	CCTCCCTCGG	101
CAAGGCCACA	ATGAACCGGG	GAGTCCCTTT	TAGGCACTTG	CTTCTGGTGC	151
TGCAACTGGC	GCTCCTCCCA	GCAGCCACTC	AGGGAAACAA	AGTGGTGCTG	201
GGCAAAAAG	GGGATACAGT	GGAAGTACC	TGTACAGCTT	CCCAGAAGAA	251
GAGCATACAA	TTCCACTGGA	AAAAGTCCAA	CCAGATAAAG	ATTCTGGGAA	301
ATCAGGGCTC	CTTCTTAACT	AAAGGTCCAT	CCAAGCTGAA	TGATCGCGCT	351
GACTCAAGAA	GAAGCCTTTG	GGACCAAGGA	AACTTCCCCC	TGATCATCAA	401
GAATCTTAAG	ATAGAAGACT	CAGATACTTA	CATCTGTGAA	GTGGAGGACC	451
AGAAGGAGGA	GGTGCAATTG	CTAGTGTTTCG	GATTGACTGC	CFACTCTGAC	501
ACCCACCTGC	TTCAGGGGCA	GAGCCTGACC	CTGACCTTGG	AGAGCCCCCC	551
TGGTAGTAGC	CCCTCAGTGC	AATGTAGGAG	TCCAAGGGGT	AAAAACATAC	601
AGGGGGGGAA	GACCCCTCTCC	GTGTCTCAGC	TGGAGCTCCA	GGATAGTGGC	651
ACCTGGACAT	GCACTGTCTT	GCAGAACCAG	AAGAAGGTGG	AGTTCAAAAT	701
AGACATCGTG	GTGCTAGCTT	TCCAGAAGGC	CTCCAGCATA	GTCTATAAGA	751
AAGAGGGGGA	ACAGGTGGAG	TTCTCCTTCC	CACTCGCCTT	TACAGTTGAA	801
AAGCTGACGG	GCAGTGGCGA	GCTGTGGTGG	CAGGCGGAGA	GGGCTTCCTC	851
CTCCAAGTCT	TGGATCACCT	TTGACCTGAA	GAACAAGGAA	GTGTCTGTAA	901
AACGGGTAC	CCAGGACCCT	AAGCTCCAGA	TGGGCAAGAA	GCTCCCGCTC	951
CACCTCACCC	TGCCCCAGGC	CTTGCCTCAG	TATGCTGGCT	CTGGAAACCT	1001
CACCTGGCC	CTTGAAGCGA	AAACAGGAAA	GTTGCATCAG	GAAGTGAACC	1051
TGGTGGTGAT	GAGAGCCACT	CAGCTCCAGA	AAAATTTGAC	CTGTGAGGTG	1101
TGGGGACCCA	CCTCCCCTAA	GCTGATGCTG	AGCTTGAAAC	TGGAGAACAA	1151
GGAGGCAAAG	GTCTCGAAGC	GGGAGAAGCC	GGTGTGGGTG	CTGAACCCTG	1201
AGGCGGGGAT	GTGGCAGTGT	CTGCTGAGTG	ACTCGGGACA	GGTCCTGCTG	1251
GAATCCAACA	TCAAGGTTCT	GCCACATGG	TCCACCCCGG	TGCACGCGGA	1301
TCCC (SEQ ID NO: 28)					

Amino Acid Sequence

MNRGVFPRHL	LLVLQLALLP	AATQGNKVVL	GKKGDTVELT	CTASQKKSIIQ	51
FHWKNSNQIK	ILGNQGSFLT	KGPSKLNDRA	DSRRSLWDQG	NFPLIIKNLK	101
IEDSDTYICE	VEDQKEEVQL	LVFGLTANS	THLLQGQSLT	LTLESPPGSS	151
PSVQCRSPRG	KNIQGGKTLS	VSQLELQDSG	TWTCTVLQNO	KKVEFKIDIV	201
VLAFAQASSI	VYKKEGEQVE	FSFPLAFTVE	KLTGSGELWW	QAERASSSKS	251
WITFDLKNKE	VSVKRVTQDP	KLQMGKKLPL	HLTLPQALPQ	YAGSGNLTLA	301
LEAKTGKLHQ	EVNLVVMRAT	QLQKNLTCEV	WGPTSPKLML	SLKLENKEAK	351
VSKREKPVWV	LNPEAGMWQC	LLSDSGQVLL	ESNIKVLPTW	STPVHADP	
(SEQ ID NO: 29)					

FIG. 23

Nucleic Acid Sequence

GCCTGTTTGA	GAAGCAGCGG	GCAAGAAAGA	CGCAAGCCCA	GAGGCCCTGC	51
CATTTCTGTG	GGCTCAGGTC	CCTACTGGCT	CAGGCCCTG	CCTCCCTCGG	101
CAAGGCCACA	ATGAACCGGG	GAGTCCCTTT	TAGGCACTTG	CTTCTGGTGC	151
TGCAACTGGC	GCTCCTCCCA	GCAGCCACTC	AGGGAAACAA	AGTGGTGCTG	201
GGCAAAAAAG	GGGATACAGT	GGAAGTGACC	TGTACAGCTT	CCCAGAAGAA	251
GAGCATACAA	TTCCACTGGA	AAAAGTCCAA	CCAGATAAAG	ATTCTGGGAA	301
ATCAGGGGCTC	CTTCTTAACT	AAAGGTCCAT	CCAAGCTGAA	TGATCGCGCT	351
GACTCAAGAA	GAAGCCTTTG	GGACCAAGGA	AACTTCCCCC	TGATCATCAA	401
GAATCTTAAG	ATAGAAGACT	CAGATACTTA	CATCTGTGAA	GTGGAGGACC	451
AGAAGGAGGA	GGTGCAATTG	CTAGTGTTTCG	GATTGACTGC	CAACTCTGAC	501
ACCCACCTGC	TTCAGGGGCA	GAGCCTGACC	CTGACCTTGG	AGAGCCCCCC	551
TGGTAGTAGC	CCCTCAGTGC	AATGTAGGAG	TCCAAGGGGT	AAAAACATAC	601
AGGGGGGGAA	GACCCTCTCC	GTGTCTCAGC	TGGAGCTCCA	GGATAGTGGC	651
ACCTGGACAT	GCACTGTCTT	GCAGAACCAG	AAGAAGGTGG	AGTTCAAAAT	701
AGACATCGTG	GTGCTAGCT	(SEQ ID NO: 30)			

Amino Acid Sequence

ENRGVPFRHL	LLVLQLALLP	AATQGNKVVL	GKKGDTVELT	CTASQKKSIIQ	51
FWKNSNQIK	ILGNQGSFLT	KGPSKLNDRA	DSRRSLWDQG	NFPLIIKNLK	101
VEDSDTYICE	VEDQKEEVQL	LVFGLTANS	THLLQGQSLT	LTLESPPGSS	151
PSVQCRSPRG	KNIQGGKTLS	VSQLELQDSG	TWTCTVLQNO	KKVEFKIDIV	201
VLA (SEQ ID NO: 31)					

FIG. 24

Hinge, CH₂, and CH₃ Domains of Human IgG1

Nucleic Acid Sequence

GCTAGCAGAG	CCCAAATCTT	GTGACAAAAC	TCACACATGC	CCACCGTGCC	51
CAGCACCTGA	ACTCCTGGGG	GGACCGTCAG	TCTTCCTCTT	CCCCCAAAA	101
CCCAAGGACA	CCCTCATGAT	CTCCCGGACC	CCTGAGGTCA	CATGCGTGGT	151
GGTGGACGTG	AGCCACGAAG	ACCCTGAGGT	CAAGTTCAAC	TGGTACGTGG	201
ACGGCGTGGA	GGTGCATAAT	GCCAAGACAA	AGCCGCGGGA	GGAGCAGTAC	251
AACAGCACGT	ACCGGGTGGT	CAGCGTCCTC	ACCGTCCTGC	ACCAGGACTG	301
GCTGAATGGC	AAGGAGTACA	AGTGCAAGGT	CTCCAACAAA	GCCCTCCCAG	351
CCCCCATCGA	GAAAACCATC	TCCAAAGCCA	AAGGGCAGCC	CCGAGAACCA	401
CAGGTGTACA	CCCTGCCCCC	ATCCCGGGAT	GAGCTGACCA	AGAACCAGGT	451
CAGCCTGACC	TGCCTGGTCA	AAGGCTTCTA	TCCCAGCGAC	ATCGCCGTGG	501
AGTGGGAGAG	CAATGGGCAG	CCGGAGAACA	ACTACAAGAC	CACGCCTCCC	551
GTGCTGGACT	CCGACGGCTC	CTTCTTCCTC	TACAGCAAGC	TCACCGTGGA	601
CAAGAGCAGG	TGGCAGCAGG	GGAACGTCTT	CTCATGCTCC	GTGATGCATG	651
AGGCTCTGCA	CAACCACTAC	ACGCAGAAGA	GCCTCTCCCT	GTCTCCGGGG	701
CTGCAACTGG	ACGAGACCTG	TGCTGAGGCC	CAGGACGGGG	AGCTGGACGG	751
GCTCTGGACG	ACGGATCC	(SEQ ID NO: 32)			

Amino Acid Sequence

EPKSCDKTHT	CPPCPAPELL	GGPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	51
VSHEDPEVKF	NWYVDGVEVH	NAKTKPREEQ	YNSTYRVVSV	LTVLHQDWLN	101
GKEYKCKVSN	KALPAPIEKT	ISKAKGQPRE	PQVYTLPPSR	DELTKNQVSL	151
TCLVKGFYPS	DIAVEWESNG	QPENNYKTPP	PVLDSGGSFF	LYSKLTVDKS	201
TRWQQGNVFSC	SVMHEALHNH	YTQKSLSLSP	GLQLDETCAE	AQDGELDGLW	251
TTDP (SEQ ID NO: 33)					

FIG. 25

CD7 Transmembrane Domain

Nucleic Acid Sequence

CCAAGGGCCT	CTGCCCTCCC	TGCCCCACCG	ACAGGCTCCG	CCCTCCCTGA	51
CCCGCAGACA	GCCTCTGCCC	TCCCTGACCC	GCCAGCAGCC	TCTGCCCTCC	101
CTGCGGGCCCT	GGCGGTGATC	TCCTTCCTCC	TCGGGCTGGG	CCTGGGGGTG	151
CGGTGTGTGC	TGGCGAGGAC	GCGT	(SEQ ID NO: 34)		

Amino Acid Sequence

PRASALPAPP	TGSALPDPQT	ASALPDPPAA	SALPAALAVI	SFLLGLGLGV	51
ACVLARTR	(SEQ ID NO: 35)				

FIG. 26

Zeta Intracellular Domain

Nucleic Acid Sequence

ACGCGTTTCA	GCAGGAGCGC	AGAGCCCCCC	GCGTACCAGC	AGGGCCAGAA	51
CCAGCTCTAT	AACGAGCTCA	ATCTAGGACG	AAGAGAGGAG	TACGATGTTT	101
TGGACAAGAG	ACGTGGCCGG	GACCCTGAGA	TGGGGGGAAA	GCCGAGAAGG	151
AAGAACCCTC	AGGAAGGCCT	GTACAATGAA	CTGCAGAAAG	ATAAGATGGC	201
GGAGGCCTAC	AGTGAGATTG	GGATGAAAGG	CGAGCGCCGG	AGGGGCAAGG	251
GGCACGATGG	CCTTTACCAG	GGTCTCAGTA	CAGCCACCAA	GGACACCTAC	301
GACGCCCTTC	ACATGCAGGC	CCTGCCCCCT	CGCTAAAGCG	GCCGC	
(SEQ ID NO: 36)					

Amino Acid Sequence

TRFSRSAEPP	AYQQGQNQLY	NELNLGRREE	YDVLDKRRGR	DPEMGGKPRR	51
KNPQEGLYNE	LQKDKMAEAY	SEIGMKGERR	RGKGHDGLYQ	GLSTATKDTY	101
DALHMQALPP	R	(SEQ ID NO: 37)			

FIG. 27